

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**



results of **BLAST**

BLASTP 2.2.9 [May-01-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

RID: 1087857020-23039-205662433234.BLASTQ4

Query=

(770 letters)

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF excluding environmental samples

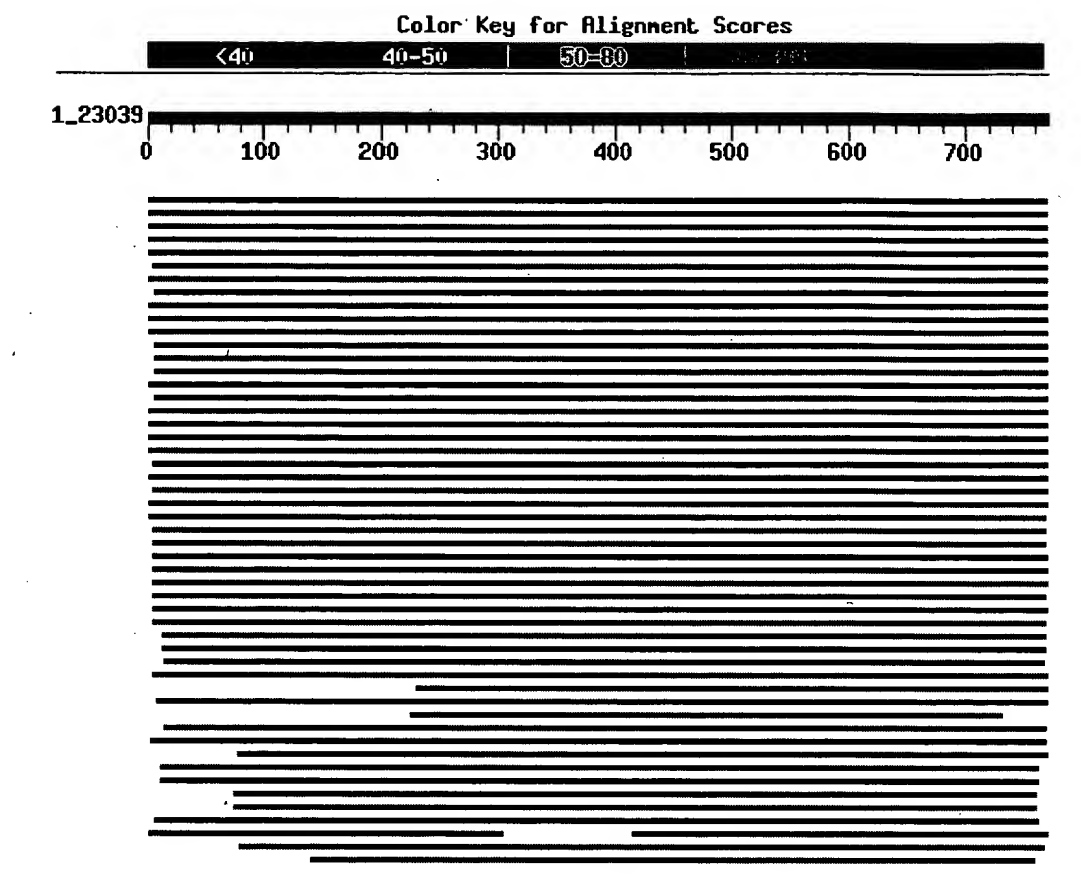
1,865,463 sequences; 619,299,334 total letters

If you have any problems or questions with the results of this search
please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Score		E	
Sequences producing significant alignments:		(bits)	Value
gi 15982958 gb AAL11507.1	vacuolar H ⁺ -pyrophosphatase [Pru...	1120	0.0
gi 3298474 dbj BAA31523.1	ovp1 [Oryza sativa]	1167	0.0
gi 2129950 pir S61423	inorganic diphosphatase (EC 3.6.1.1)...	1194	0.0
gi 15982956 gb AAL11506.1	vacuolar H ⁺ -pyrophosphatase [Pru...	1186	0.0
gi 38488588 dbj BAD02276.1	vacuolar proton pyrophosphatase...	1144	0.0
gi 322841 pir JC1466	inorganic diphosphatase (EC 3.6.1.1) ...	1154	0.0
gi 3608171 dbj BAA33149.1	proton-translocating inorganic p...	1182	0.0
gi 7436046 pir T14563	inorganic diphosphatase (EC 3.6.1.1)...	1202	0.0
gi 2129948 pir S61424	inorganic diphosphatase (EC 3.6.1.1)...	1172	0.0
gi 1103712 emb CAA58700.1	inorganic pyrophosphatase [Nicot...	1180	0.0
gi 7436041 pir S72526	inorganic diphosphatase (EC 3.6.1.1)...	1169	0.0

[gi|31580801|gb|AAP55210.1](#) vacuolar proton-inorganic pyroph... [1132](#) 0.0
[gi|7739779|gb|AAF69010.1](#) H⁺-pyrophosphatase [*Vitis vinifera*] [1109](#) 0.0
[gi|7436042|pir||S72527](#) inorganic diphosphatase (EC 3.6.1.1)... [1146](#) 0.0
[gi|30027157|gb|AAP06752.1](#) vacuolar proton-inorganic pyroph... [1166](#) 0.0
[gi|18086404|gb|AAL57660.1](#) At1g15690/F7H2_3 [*Arabidopsis th...*] [1315](#) 0.0
[gi|542059|pir||S42893](#) inorganic diphosphatase (EC 3.6.1.1) ... [1197](#) 0.0
[gi|25901033|dbj|BAC41250.1](#) vacuolar proton-inorganic pyrop... [1188](#) 0.0
[gi|22532391|gb|AAM97920.1](#) vacuolar proton-pumping PPase [C... [1179](#) 0.0
[gi|7436047|pir||T14564](#) inorganic diphosphatase (EC 3.6.1.1)... [1168](#) 0.0
[gi|11527561|dbj|BAB18681.1](#) vacuolar proton-inorganic pyrop... [1157](#) 0.0
[gi|3402487|dbj|BAA32210.1](#) Vacuolar proton pyrophosphatase ... [1311](#) 0.0
[gi|45479863|gb|AAS66771.1](#) PPase [*Hevea brasiliensis*] [1207](#) 0.0
[gi|2827755|sp|P21616|AVP3_PHAAU](#) Pyrophosphate-energized vac... [1171](#) 0.0
[gi|41023649|emb|CAF18416.1](#) proton translocating pyrophosph... [1140](#) 0.0
[gi|38045977|gb|AAR08913.1](#) pyrophosphate-energized vacuolar... [1279](#) 0.0
[gi|38488590|dbj|BAD02277.1](#) vacuolar proton pyrophosphatase... [1175](#) 0.0
[gi|2129949|pir||S61422](#) inorganic diphosphatase (EC 3.6.1.1)... [1190](#) 0.0
[gi|18274925|sp|Q06572|AVP3_HORVU](#) Pyrophosphate-energized va... [1153](#) 0.0
[gi|7436043|pir||T07801](#) probable inorganic diphosphatase (EC... [1178](#) 0.0
[gi|15218279|ref|NP_173021.1](#) pyrophosphate-energized vacuol... [1316](#) 0.0
[gi|1076627|pir||S54172](#) inorganic diphosphatase (EC 3.6.1.1)... [1203](#) 0.0
[gi|19310433|gb|AAL84953.1](#) At1g15690/F7H2_3 [*Arabidopsis th...*] [1314](#) 0.0
[gi|34894952|ref|NP_908801.1](#) putative H⁺-pyrophosphatase [O... [994](#) 0.0
[gi|33465893|gb|AAQ19328.1](#) H⁺-pyrophosphatase [*Oryza sativa*... [991](#) 0.0
[gi|4126976|dbj|BAA36841.1](#) vacuolar H⁺-pyrophosphatase [Cha... [941](#) 0.0
[gi|45267862|gb|AAS55761.1](#) putative inorganic diphosphatase... [937](#) 0.0
[gi|2118183|pir||S61425](#) inorganic diphosphatase (EC 3.6.1.1)... [881](#) 0.0
[gi|14970742|emb|CAC44451.1](#) proton-translocating inorganic ... [833](#) 0.0
[gi|1049255|gb|AAA80347.1](#) H⁺-pyrophosphatase [815](#) 0.0
[gi|21654895|gb|AAK95376.1](#) vacuolar-type proton translocati... [692](#) 0.0
[gi|8886133|gb|AAF80381.1](#) vacuolar-type proton translocatin... [681](#) 0.0
[gi|24214171|ref|NP_711652.1](#) Pyrophosphate-energized vacuol... [646](#) 0.0
[gi|13661740|gb|AAK38077.1](#) H⁺-translocating inorganic pyrop... [611](#) e-173
[gi|13661738|gb|AAK38076.1](#) H⁺-translocating inorganic pyrop... [610](#) e-173
[gi|23509763|ref|NP_702430.1](#) V-type H(+)-translocating pyro... [585](#) e-165
[gi|4324984|gb|AAD17215.1](#) proton-pumping vacuolar pyrophosp... [585](#) e-165
[gi|23483521|gb|EAA19163.1](#) V-type H(+)-translocating pyroph... [582](#) e-165

[gi|14149007|emb|CAC39165.1](#) vacuolar-type H⁺-pyrophosphatas... [570](#) e-161
[gi|28210139|ref|NP_781083.1](#) vacuolar-type H⁺-pyrophosphata... [513](#) e-144
[gi|20092675|ref|NP_618750.1](#) inorganic pyrophosphatase [Met... [483](#) e-135
[gi|33301196|sp|Q8TJA9|HPP1_METAC](#) Pyrophosphate-energized pr... [483](#) e-135
[gi|21226802|ref|NP_632724.1](#) vacuolar-type H⁺-pyrophosphata... [482](#) e-134
[gi|5708065|dbj|BAA83103.1](#) inorganic pyrophosphatase [Aceta... [472](#) e-131
[gi|34762889|ref|ZP_00143872.1](#) Inorganic pyrophosphatase [F... [457](#) e-127
[gi|19705321|ref|NP_602816.1](#) Inorganic pyrophosphatase [Fus... [455](#) e-126
[gi|15642948|ref|NP_227989.1](#) pyrophosphatase, proton-transl... [446](#) e-123
[gi|1076628|pir||S54173](#) inorganic diphosphatase (EC 3.6.1.1)... [442](#) e-122
[gi|39998380|ref|NP_954331.1](#) V-type H⁽⁺⁾-translocating pyro... [439](#) e-121
[gi|48845538|ref|ZP_00299816.1](#) COG3808: Inorganic pyrophosp... [434](#) e-120
[gi|21226803|ref|NP_632725.1](#) vacuolar-type H⁺-pyrophosphata... [431](#) e-119
[gi|48838581|ref|ZP_00295523.1](#) COG3808: Inorganic pyrophosp... [431](#) e-119
[gi|30249887|ref|NP_841957.1](#) Inorganic H⁺ pyrophosphatase [... [429](#) e-118
[gi|41723517|ref|ZP_00150444.1](#) COG3808: Inorganic pyrophosp... [428](#) e-118
[gi|48764244|ref|ZP_00268796.1](#) COG3808: Inorganic pyrophosp... [427](#) e-118
[gi|33301139|sp|O68460|HPPA_RHORU](#) Pyrophosphate-energized pr... [426](#) e-118
[gi|46201733|ref|ZP_00054472.2](#) COG3808: Inorganic pyrophosp... [426](#) e-117
[gi|45530368|ref|ZP_00181500.1](#) COG3808: Inorganic pyrophosp... [425](#) e-117
[gi|33301186|sp|Q8KY01|HPP2_RHOPA](#) Pyrophosphate-energized pr... [420](#) e-116
[gi|22971000|ref|ZP_00018005.1](#) hypothetical protein [Chloro... [418](#) e-115
[gi|20092676|ref|NP_618751.1](#) inorganic pyrophosphatase [Met... [418](#) e-115
[gi|20806805|ref|NP_621976.1](#) vacuolar-type H⁺-translocating... [416](#) e-115
[gi|27380137|ref|NP_771666.1](#) H⁺ translocating pyrophosphate... [416](#) e-114
[gi|29348820|ref|NP_812323.1](#) pyrophosphate-energized vacuol... [412](#) e-113
[gi|47575275|ref|ZP_00245310.1](#) COG3808: Inorganic pyrophosp... [408](#) e-112
[gi|21244165|ref|NP_643747.1](#) H⁺ translocating pyrophosphate... [408](#) e-112
[gi|15888511|ref|NP_354192.1](#) AGR_C_2169p [Agrobacterium tum... [403](#) e-110
[gi|17935080|ref|NP_531870.1](#) H⁺ translocating pyrophosphate... [402](#) e-110
[gi|15219362|ref|NP_173122.1](#) vacuolar-type H⁺-translocating... [402](#) e-110
[gi|42523211|ref|NP_968591.1](#) vacuolar-type H⁺-pyrophosphata... [402](#) e-110
[gi|15964971|ref|NP_385324.1](#) PROBABLE H⁺ TRANSLOCATING PYRO... [400](#) e-110
[gi|45915706|ref|ZP_00194428.2](#) COG3808: Inorganic pyrophosp... [399](#) e-109
[gi|25290360|pir||H96818](#) hypothetical protein F9K20.2 [impor... [397](#) e-109
[gi|13476947|ref|NP_108517.1](#) H⁺ translocating pyrophosphate... [397](#) e-109
[gi|18412180|ref|NP_565195.1](#) vacuolar-type H⁺-translocating... [396](#) e-109

[gi|6901676|gb|AAF31163.1](#) vacuolar-type H⁺-translocating in... [396](#) e-109
[gi|48851197|ref|ZP_00305439.1](#) COG3808: Inorganic pyrophosp... [395](#) e-108
[gi|21232741|ref|NP_638658.1](#) H⁺ translocating pyrophosphate... [393](#) e-107
[gi|48858370|ref|ZP_00312326.1](#) COG3808: Inorganic pyrophosp... [392](#) e-107
[gi|17987468|ref|NP_540102.1](#) H⁺ TRANSLOCATING PYROPHOSPHATE... [390](#) e-107
[gi|23501658|ref|NP_697785.1](#) V-type H⁽⁺⁾-translocating pyro... [387](#) e-106
[gi|33301205|sp|Q8YGH4|HPPA_BRUME](#) Pyrophosphate-energized pr... [387](#) e-106
[gi|18419442|gb|AAL69328.1](#) inorganic pyrophosphatase [Bruce... [383](#) e-105
[gi|39935798|ref|NP_948074.1](#) H⁺ translocating pyrophosphate... [379](#) e-103
[gi|18419444|gb|AAL69329.1](#) inorganic pyrophosphatase [Sinor... [377](#) e-103
[gi|23479810|gb|EAA16540.1](#) vacuolar-type H⁺ pumping pyropho... [372](#) e-101
[gi|16125612|ref|NP_420176.1](#) proton pump, putative [Cauloba... [371](#) e-101
[gi|48835222|ref|ZP_00292223.1](#) COG3808: Inorganic pyrophosp... [347](#) 7e-94
[gi|29831159|ref|NP_825793.1](#) putative inorganic H⁺ pyrophos... [344](#) 4e-93
[gi|18312865|ref|NP_559532.1](#) vacuolar-type H⁺-pyrophosphata... [343](#) 7e-93

Alignments

☐ [>gi|15982958|gb|AAL11507.1](#) vacuolar H⁺-pyrophosphatase [*Prunus persica*]
 Length = 759

Score = 1120 bits (2898), Expect = 0.0

Identities = 608/767 (79%), Positives = 662/767 (86%), Gaps = 10/767 (1%)

Query: 5 ALLPELWTEILVPICAVIGIAFSLFQWYVVS RVKLTSDLXXXXXXXXXXXXXXXXXXDYLI-63

LL E T++L+P+ A++G+AF+L QW++VSRVK++ D LI

Subjt: 2 GLLSEGLTQLLIPLAALVGLAFALLQWFLVSRVKVSGS-----YGEENG YKDKLIG 52

Query: 64

EEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKXXXXXXXXXXXXXXXXXXLGSVEGFST 123

E EEGV+ V K AEIQ AIS GATSFLFT+Y+Y LGSV+GFST

Sbjct: 53 EAEEGVDSLEVTIKVAEIQNAISIGATSFLFTQYRYLSIFVGVFSAIIFLFLGSVKGFST
112

Query: 124

DNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGV 183
++PCTY+T TCKPALA A F+TIAF+LGA+TSVLSGF GMKIATYANARTTLEAR+GV

Sbjct: 113

KSEPCTYNTGNTCKPALANALFTTIAFLLGALTSVLSGFFGMKIATYANARTTLEARRGV 172

Query: 184

GKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMAL 243
GKAFI AFRSGAVMGFLLAA+GLLVLYITIN+FK+YYGDDWEGL+E+ITGYGLGGSSMAL

Sbjct: 173

GKAFITAFRSGAVMGFLLAANGLLVLYITINLFKLYYGDDWEGLYESITGYGLGGSSMAL 232

Query: 244

FGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSY 303

FGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSY

Sbjct: 233

FGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSY 292

Query: 304 AEASCAALVVASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEIEP
363

AE+SCAAL VASISSFGI+HD+TAM YPL+ISSMGI+VCLITTLFATD FEIK V EIEP

Sbjct: 293 AESSCAALFVASISSFGISHDYTAMSYP LISSMGIVVCLITTLFATDLFEIKKVNEIEP
352

Query: 364 ALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVKNWQLFLCVCVGLWAGLIIG
423

+LK QL+ISTV+MT GIA V++V LP+ FT+F FGT K VKNW LF CV +GLWAGL+IG

Sbjct: 353

SLKRQLLISTVLMTAGIAAVTFVALPSEFTLFQFGTNKAVKNWYLFFCVAIGLWAGLVIG 412

Query: 424

FVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXXM 483
+ TEY+TSNAYSPVQDVADSCRTGAATNVIFGLALGYK M

Sbjct: 413 YTTEYHTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIIPVFAIAFAIYVSFSLAAM
472

Query: 484

YGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAI 543

YG+AVAALGMLSTI+TGLAIDAYGPISDNAGGIAEMAGMSH IRERTDALDAAGNTTAAI

Sbjct: 473 YGIAVAALGMLSTISTGLAIDAYGPISDNAGGIAEMAGMSHEIRERTDALDAAGNTTAAI
532

Query: 544

GKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTTPKVIIIGLLVGAMLPYWFSAMTMKSVGS 603

GKGFAIGSAALVSLALFGA+VSRAGI TVDVLTTPKV IGLLVGAMLPYWFSAMTMKSVGS

Sbjct: 533

GKGFAIGSAALVSLALFGAYVSRAGIETVDVLTTPKVFIGLLVGAMLPYWFSAMTMKSVGS 592

Query: 604

AALKMVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFF 663

AALKMVEEVRQFNTIPGLMEGTAKPDYATCVKISTDAS+KEMIPPG LVMLTPLI G F

Sbjct: 593

AALKMVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASLKEMIPPGALVMLTPLIAGTF 652

Query: 664

FGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAksLGPKGSEPHKAA 723

FGVETL+G+LAGSLVSGVQIAISASNTGGAWDNAKKYIEAG SEHAksLGPKGS+PHKAA

Sbjct: 653

FGVETLAGILAGSLVSGVQIAISASNTGGAWDNAKKYIEAGASEHAksLGPKGSDPHKAA 712

Query: 724 VIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

VIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFA HGG+LFK+

Sbjct: 713 VIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFAAHGGVLFKWL 759



>gi|3298474|dbj|BAA31523.1| ovp1 [Oryza sativa]

Length = 771

Score = 1167 bits (3019), Expect = 0.0

Identities = 633/769 (82%), Positives = 674/769 (87%), Gaps = 3/769 (0%)

Query: 5 ALLPELWTEILVPICAVIGIAFSLFQWYVVS RVKLTSDLXXXXXXXXXXXXXXXXXX---DY
61

A+LP+L T++LVP AV+GIAF++ QW +VS+VK+T++ +Y

Sbjct: 3

AILPDLATQVLVPAAAVVGIAFAVVQWVLVSKVKMTAERRGGEGSPGAAAGKDGGAASEY 62

Query: 62

LIEEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXX LGSVEGF 121

LIEEEEG+N+ +VV KC+EIQ AISEGATSFLFTEYKY LGSVEGF

Sbjct: 63 LIEEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYVGLFMGIFAVLIFLFLGSVEGF
122

Query: 122

STDNKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARK 181

ST ++PC Y R CKPALA A FST+AFVLGAVTS++SGFLGMKIATYANARTTLEARK

Sbjct: 123

STKSQPCHYSKDRMCKPALANAIFSTVAFVLGAVTSVLSGFLGMKIATYANARTTLEARK 182

Query: 182

GVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSM 241

GVGKAFI AFRSGAVMGFLLAASGL+VLYI IN+F IYYGDDWEGLFEAITGYGLGGSSM

Sbjct: 183

GVGKAFITAFRSGAVMGFLLAASGLVLYIAINLFGIYYGDDWEGLFEAITGYGLGGSSM 242

Query: 242

ALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG 301

ALFGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG

Sbjct: 243

ALFGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG 302

Query: 302 SYAEASCAALVVASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEI
361

SYAE+SCAALVVASISSFGINH+FT M YPLLISS+GI+ CLITTLFATDFFEIK V EI

Sbjct: 303 SYAESSCAALVVASISSFGINHEFTPMLYPLLISSVGIIACLITTLFATDFFEIKAVDEI 362

Query: 362

EPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGLI 421

EPALK QLIISTV+MTVGI +VSW+GLP SFTIFNFG QK V NWQLFLCV VGLWAGLI

Sbjct: 363

EPALKKQLIISTVVMTVGIVLVS WLGLPYSTIFNFGAQKTVYNWQLFLCVAVGLWAGLI 422

Query: 422

IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXX 481

IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 423 IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAFSIFLSFSLA
482

Query: 482

XMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA 541

MYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA

Sbjct: 483

AMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA 542

Query: 542

AIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMKSV 601

AIGKGFAIGSAALVSLALFGAFVSRA I TVDVLT PKV IGL+VGAMLPYWFSAMTMKSV

Sbjct: 543

AIGKGFAIGSAALVSLALFGAFVSRAAISTVDVLT PKVFIGLIVGAMLPYWFSAMTMKSV 602

Query: 602

GSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVG 661

GSAALKMVEEVRRQFN+IPGLMEGT KPDYATCVKISTDASIKEMIPPG LVML+PLIVG

Sbjct: 603

GSAALKMVEEVRRQFNSIPGLMEGTTKPDYATCVKISTDASIKEMIPPGALVMLSPLIVG 662

Query: 662

FFFGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHK 721

FFGVETLSG+LAG+LVSGVQIAISASNTGGAWDNAKKYIEAG SEHA++LGPKGS+ HK

Sbjct: 663

IFFGVETLSGLLAGALVSGVQIAISASNTGGAWDNAKKYIEAGASEHARTLGPKGSDCHK 722

Query: 722 AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFK+F

Sbjct: 723 AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKWF 771

☐ >gj|2129950|pir||S61423 inorganic diphosphatase (EC 3.6.1.1) (clone TVP9) - common tobacco

Length = 765

Score = 1194 bits (3088), Expect = 0.0

Identities = 647/769 (84%), Positives = 683/769 (88%), Gaps = 4/769 (0%)

Query: 2 VAPALLPELWTEILVPICAVIGIAFSLFQWYVVS RVKLTSDLXXXXXXXXXXXXXXXXXXXXDY
61

+ ALLP+L EI++P+CAVIGI FSL QWY+VS VKLT + DY

Sbjct: 1 MGAALLPDLGAEIVIPVCAVIGIVFSLVQWYLVSNVKLTPE----SSSPSNNGKNGYGDY
56

Query: 62

LIEEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXXXXXLGSVEGF 121

LIEEEEG+N+Q+VV KCAEIQ AISEGATSFLFT Y+Y LGSVEGF

Sbjct: 57 LIEEEEGINEQNWWKCAEIQNAISEGATSFLFTTYQYVGIFMIAFAILIFLFLGSVEGF
116

Query: 122

STDNKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARK 181

ST ++PCTY+ + CKPALATA FST++F+LGAVTSV+SGFLGMKIATYANARTTLEARK

Sbjct: 117

STKSQPCTYNKEKLCKPALATAIFSTVSFLLGAVTSVWSGFLGMKIATYANARTTLEARK 176

Query: 182

GVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSM 241

GVGKAFIVAFRSGAVMGFLLAA+GLLVLYI IN+FK+YYGDDWEGLFEAITGYGLGGSSM

Sbjct: 177

GVGKAFIVAFRSGAVMGFLLAANGLLVLYIAINLFKLYYGDDWEGLFEAITGYGLGGSSM 236

Query: 242

ALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG 301

ALFGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG

Sbjct: 237

ALFGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG 296

Query: 302 SYAEASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEI

361

SYAEASCAALVVASISSFGINH+FTAM YPLLISSMGIL+CLITTLFATDFFEIK VKEI

Sbjct: 297 SYAEASCAALVVASISSFGINHEFTAMLYPLLISSMGILICLITTLFATDFFEIKAVKEI 356

Query: 362

EPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGLI 421

EPALKNQLIIST +MTVGIAIV+W LP+SFTIFNFG QKVVKNWQLFLCV VGLWAGLI

Sbjct: 357 EPALKNQLIISTALMTVGIAIVTWTCLPSSFTIFNFGAQKVVKNWQLFLCVAVGLWAGLI

416

Query: 422

IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXX 481

IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 417 IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAIAIFVSFSFA

476

Query: 482

XMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA 541

M +AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA

Sbjct: 477

AMGYIAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA 536

Query: 542

AIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMKSV 601

AIGKGFAIGSAALVSLALFGAFVSRA I TVDVLTP+V IGL+VGAMLPYWFSAMTMKSV

Sbjct: 537

AIGKGFAIGSAALVSLALFGAFVSRAAITTVDVLTPQVFIGLIVGAMLPYWFSAMTMKSV 596

Query: 602

GSAALKMVVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVG 661
GSAALKMVVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPG LVMLTPLIVG

Sbjct: 597

GSAALKMVVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGALVMLTPLIVG 656

Query: 662

FFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAWSLGPKESEPHK 721
FFFGVETLSGVLAG+LVSGVQIAISASNTGGAWDNAKKYIEAG SEHA++LGPKEG+PHK

Sbjct: 657

IFFGVETLSGVLAGALVSGVQIAISASNTGGAWDNAKKYIEAGASEHARTLGPKEGSDPHK 716

Query: 722 AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGG+LFK F

Sbjct: 717 AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGLLFKIF 765



>gi|15982956|gb|AAL11506.1| vacuolar H⁺-pyrophosphatase [Prunus persica]

Length = 767

Score = 1186 bits (3068), Expect = 0.0

Identities = 645/765 (84%), Positives = 682/765 (89%), Gaps = 1/765 (0%)

Query: 6 LLPELWTEILVPICAVIGIAFSLFQWYVVSrvKLTSDLXXXXXXXXXXXXXXXXXXDYLIEE
65

LL L TEI++P+ AVIGI FSL QW++VSRVK+T + DYLIEE

Sbjct: 4 LLSTLATEIVIPVAAVIGIVFSLVQWFIVSRVKVTLE-RHAPPAGPNSNKNGFNDYLIEE 62

Query: 66

EEGVNDQSWAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXXXLGSVEGFSTDN 125

EEG++DQ+VWAKCAEIQTASEGATSFLFTEY+Y LGSVEGFST +

Sbjct: 63 EEGLHDQNVWAKCAEIQTASEGATSFLFTEYQYVGVMVVFALIFLFLGSVEGFSTKS
122

Query: 126

KPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVGK 185

+PCTYD RTCKPALATA FST+AFVLG VTS+LSGFLGMKIATYANARTTLEARKGVGK

Sbjct: 123

QPCTYDAQRTCKPALATAIFSTVAFVLGGVTSILSGFLGMKIATYANARTTLEARKGVGK 182

Query: 186

AFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMALFG 245

AFIVAFRSGAVMGFLLAA+GLLVLYITINVFK+YYGDDWEGLFE+ITGYGLGGS+MALFG

Sbjct: 183

AFIVAFRSGAVMGFLLAANGLLVLYITINVFKVYYGDDWEGLFESITGYGLGGSAMALFG 242

Query: 246

RVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE 305

RVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE

Sbjct: 243

RVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE 302

Query: 306 ASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEIEPAL

365

+SCAALVVASISSFGINH+FT+M YPLLISSMGIL+CLITTLFATDFFEIK VKEIEPAL

Sbjct: 303 SSCAALVVASISSFGINHEFTSMLYPLLISSMGILICLITTLFATDFFEIKAVKEIEPAL 362

Query: 366 KNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKWQFLCVCVGLWAGLIIGFV

425

K QLIISTV+MTVGIAI+SW+ LP+SFTI+NFG QKVVKWQFLFCV VGLWAGLIIGFV

Sbjct: 363 KKQLIISTVLMTVGIAIISWIALPSSFTIYNFGVQKVVKWQFLCVAVGLWAGLIIGFV

422

Query: 426

TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXMYG 485

TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK MYG

Sbjct: 423 TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAVSIFVSFSFAAMYG

482

Query: 486

VAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIGK 545
+AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIGK

Sbjct: 483

IAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIGK 542

Query: 546

GFAIGSAALVSLALFGAFVSRAGIHTVDVLTTPKVIIGLLVGAMLPYWFSAMTMKSVGSAA 605
GFAIGSAALVSLALFGAFVSRAI TVDVLTTPKV IGL+VGAMLP FSAMTMKSVGSAA

Sbjct: 543

GFAIGSAALVSLALFGAFVSRAAISTVDVLTTPKVFIGLIVGAMLPTGFSAMTMKSVGSAA 602

Query: 606

LKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFFFG 665
LKMVEEVRRQFNTIPGLMEGTAKP YATCVKISTDASIKEMIPPG LV+LTPLIVG FG

Sbjct: 603 LKMVEEVRRQFNTIPGLMEGTAKPSYATCVKISTDASIKEMIPPGALVILTPLIVGTLFG
662

Query: 666

VETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHKAAVI 725
VETLSGVLAGSLVSGVQ+AISASNTGGAWDNAKKYIEAG SEHA++LGPKGS+PHKAAVI

Sbjct: 663

VETLSGVLAGSLVSGVQVAISASNTGGAWDNAKKYIEAGASEHARTLGPKGSDPHKAAVI 722

Query: 726 GDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

GDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGG+LFK F

Sbjct: 723 GDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGLLFKIF 767

❑ >gj|38488588|dbj|BAD02276.1| vacuolar proton pyrophosphatase [Oryza sativa (japonica
cultivar-group)]

Length = 762

Score = 1144 bits (2958), Expect = 0.0

Identities = 621/766 (81%), Positives = 667/766 (87%), Gaps = 5/766 (0%)

Query: 5 ALLPELWTEILVPICAVIGIAFSLFQWYVVS RVKLTSDLXXXXXXXXXXXXXXXXXXDY LIE
64

A+L ++ TE+L+PI A+IGI FS+ QW +V+RVKL D LIE

Sbjct: 2 AILSDVATEVLIPIAAIIGIGFSIAQWVLVARVKLAPS-----QPGASRSKDGYGDSLIE 56

Query: 65

EEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXXXLGSVEGFSTD 124

EEEG+ND +VAKCAEIQ AI+EGATSFLFTEY+Y LGSVEGFST

Sbjct: 57 EEEGLNDHNWVAKCAEIQNAIAEGATSFLFTEYQYGVFMSIFAVWIFLFLGSVEGFSTK
116

Query: 125

NKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLGFLGMKIATYANARTTLEARKGVG 184

PCTY + CKPAL A FST++F+LGA+TSV+SGFLGMKIATYANARTTLEARKGVG

Sbjct: 117

THPCTYSKDKECKPALFNALFSTVSFLLGAITSVSVSGFLGMKIATYANARTTLEARKGVG 176

Query: 185

KAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMALF 244

KAFI AFRSGAVMGFLLA++GLLVLYI IN+FK+YYGDDWEGLFE+ITGYGLGGSSMALF

Sbjct: 177

KAFITAFRSGAVMGFLLASNGLLVLYIAINLFKMYYGDDWEGLFESITGYGLGGSSMALF 236

Query: 245

GRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYA 304

GRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYA

Sbjct: 237

GRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYA 296

Query: 305 EASCAALVWASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEIEPA
364

E+SCAALVWASISSFGINHDT MCYPLL+SSMGI+VCLITTLFATDFFEIK VKEIEP+

Sbjct: 297 ESSCAALVWASISSFGINHDTGMCYPLLSSMGIIVCLITTLFATDFFEIKAVKEIEPS
356

Query: 365 LKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGLIIGF
424

LK QLIIST +MTVGIA+VSW+ LP FTIFNFG QK V NW LFLCV +GLWAGLIIG+
Sbjct: 357 LKKQLIISTALMTVGIALVSWLALPYKFTIFNFGGEQKEVTNWGLFLCVSIGLWAGLIIGY
416

Query: 425

VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXMY 484
VTEYYTSNAYSPVQDVAD+CRTGAATNVIFGLALGYK MY
Sbjct: 417 VTEYYTSNAYSPVQDVADACRTGAATNVIFGLALGYKSVIPIFAIALGIYVSFTIAAMY
476

Query: 485

GVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIG 544
G+AVAALGMLSTIATGL+IDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIG
Sbjct: 477
GIAVAALGMLSTIATGLSIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIG 536

Query: 545

KGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMKSVGSA 604
KGFAIGSAALVSLALFGAFVSRAG+ VDL+PKVIIGL+VGAMLPYWFSAMTMKSVGSA
Sbjct: 537
KGFAIGSAALVSLALFGAFVSRAGVKVVDVLS PKVIIGLIVGAMLPYWFSAMTMKSVGSA 596

Query: 605

ALKMVVEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFF 664
ALKMVVEVRRQFNTIPGLMEGT KPDYA CVKISTDASIK+MIPPG LVMLTPLIVG F
Sbjct: 597
ALKMVVEVRRQFNTIPGLMEGTGKPDYANCVKISTDASIKQMIPPGALVMLTPLIVGTLF 656

Query: 665

GVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA KSLGPKGSEPHKAAV 724
GV+TLSGVLG+LVSGVQ+AISASNTGGAWDNAKKYIEAG SEHA+SLGPKGS+ HKA AV
Sbjct: 657
GVQTLSGVLGALVSGVQVAISASNTGGAWDNAKKYIEAGASEHARS LGPKGSDCHKAAV 716

Query: 725 IGD TIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

IGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFK F
Sbjct: 717 IGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKLF 762

☐ >gi|322841|pir|JC1466 inorganic diphosphatase (EC 3.6.1.1) - barley
Length = 761

Score = 1154 bits (2985), Expect = 0.0
Identities = 624/765 (81%), Positives = 671/765 (87%), Gaps = 6/765 (0%)

Query: 5 ALLPELWTEILVPICAVIGIAFSLFQWYVVSrvKLTSDLXXXXXXXXXXXXXXXXXXDYIE
64

A+L EL TEIL+P+C VIGI F++ QW++VS+VK+T DYIE

Sbjct: 2 AILGELGTEILIPVCGVIGIVFAVAQWFIVSKVKVTP----GALRRRRRAKNGYGDYIE 56

Query: 65
EEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXLGSVEGFSTD 124

EEEG+ND +VV KCAEIQTASEGATSFLFT Y+Y LGS+EGFST

Sbjct: 57 EEEGLNDHNWVKCAEIQTASEGATSFLFTMYQYVGMFMVFAAIIFLGSIIEGFSTK
116

Query: 125
NKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLGFLGMKIATYANARTTLEARKGVG 184

+PCTY + TCKPAL TA FST +F+LGA+TS++SGFLGMKIATYANARTTLEARKGVG

Sbjct: 117 GQPCTY-
SKGTCKPALYTALFSTASFLGAIISLVSGFLGMKIATYANARTTLEARKGVG 175

Query: 185
KAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMALF 244

KAFI AFRSGAVMGFLL++SGL+VLYITINVFK+YYGDDWEGLFE+ITGYGLGGSSMALF

Sbjct: 176
KAFITAFRSGAVMGFLLSSSGLVLYITINVFKMYGDDWEGLFESITGYGLGGSSMALF 235

Query: 245
GRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYA 304

GRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYA

Sbjct: 236

GRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYA 295

Query: 305 EASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEIEPA
364

E+SCAALVVASISSFGINHDFTAMCYPLL+SS+GI+VCL+TTLFATDFFEIK EIEPA

Sbjct: 296 ESSCAALVVASISSFGINHDFTAMCYPLLVS SVGIIVCLLTTLFATDFFEIKAANEIEPA
355

Query: 365 LKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVKNWQLFLCVCVGLWAGLIIGF
424

LK QLIIST +MTVG+A++SW+ LP FTIFNFG QK V NW LF CV VGLWAGLIIGF

Sbjct: 356 LKKQLIISTALMTVGVAVISWLALPAKFTIFNFGAQKEVSNWGLFFCVAVGLWAGLIIGF
415

Query: 425

VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXXMY 484

VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK MY

Sbjct: 416 VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAVSIYVSFSIAAMY
475

Query: 485

GVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIG 544

G+A+AALGMLST+ATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIG

Sbjct: 476

GIAMAALGMLSTMATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIG 535

Query: 545

KGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMKSVGSA 604

KGFAIGSAALVSLALFGAFVSRAG+ VDL+PKV IGL+VGAMLPYWFSAMTMKSVGSA

Sbjct: 536

KGFAIGSAALVSLALFGAFVSRAGVKVVDVLS PKVFIGLIVGAMLPYWFSAMTMKSVGSA 595

Query: 605

ALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFF 664

ALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPG LVMLTPLIVG F
Sbjct: 596
ALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGALVMLTPLIVGTLF 655

Query: 665
GVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA⁺SLGPKGSEPHKAAV 724
GVETLSGVLAG+LVSGVQIAISASNTGGAWDNAKKYIEAG SEHA+SLGPKGS+ HKAAV
Sbjct: 656
GVETLSGVLAGALVSGVQIAISASNTGGAWDNAKKYIEAGNSEHARSLGPKGSDCHKAAV 715

Query: 725 IGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKY 769
IGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFAT+GG+LFKY
Sbjct: 716 IGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATYGGLLFKY 760

☐ [>gi|3608171|dbj|BAA33149.1|](#) proton-translocating inorganic pyrophosphatase [Cucurbita
moschata]
Length = 768

Score = 1182 bits (3058), Expect = 0.0
Identities = 638/765 (83%), Positives = 676/765 (88%), Gaps = 1/765 (0%)

Query: 6 LLPELWTEILVPICAVIGIAFSLFQWYVVS⁺RVKLTSDLXXXXXXXXXXXXXXXXXXXXDYLIEE
65
+LP+L TEI +P+CAVIGI FSL QWY VS+VKL+ DYLIEE
Sbjct: 5 ILPDLGTEIFIPVCAVIGIVFSLVQWYVVSQVKLSPG-RDAAHNNSAGSKNGYS⁺DYLIEE
63

Query: 66
EEGVNDQSWAKCAEIQT⁺AISEGATSFLFTEYKYXXXXXXXXXXXXXXXXXXLGSVEGFSTDN 125
EEGVND +VV KCAEIQ+AISEGATSFLFTEYKY LGSVE FST
Sbjct: 64 EEGVNDHN⁺VIKCAEIQSAISEGATSFLFTEYKYVGIFMVLF⁺AVLIFVFLGSVESFSTKP
123

Query: 126

KPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVGK 185
+PCTYD TRTCKPALATA FST++F+LGAVTSV+SGFLGMKIATYANARTTLEARKGVGK

Sbjct: 124

QPCTYDKTRTCKPALATAIFSTVSFLLGAVTSVVSFGFLGMKIATYANARTTLEARKGVGK 183

Query: 186

AFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMALFG 245
AFI AFRSGAVMGFLLAA+GLLV+I IN+FK+YYGDDW GLFE+ITGYGLGGSSMALFG

Sbjct: 184

AFITAFRSGAVMGFLLAANGLLVLFIAINLFKLYYGDDWGGLFESITGYGLGGSSMALFG 243

Query: 246

RVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE 305

RVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE

Sbjct: 244

RVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE 303

Query: 306 ASCAALVVASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEIEPAL
365

+SCAALVVASIS FG NH+ T M YPL++SSMGILVCLITTLFATDFFEIK VKEIEPAL

Sbjct: 304 SSCAALVVASISPFGNNHELTPMLYPLIVSSMGILVCLITTLFATDFFEIKAVKEIEPAL
363

Query: 366 KNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVKNWQLFLCVCVGLWAGLIIGFV
425

K QLIISTV+MT GIAIV+W+ +P+SFTIFNFGTQKV NW+LFLCV VGLWAGLIIGFV

Sbjct: 364 KKQLIISTVLMTFGIAIVTWLSVPSSFTIFNFGTQKVVTNWKLFLCVAVGLWAGLIIGFV
423

Query: 426

TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXMYG 485
TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK MYG

Sbjct: 424 TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAVSIFVSFTFAAMYG
483

Query: 486

VAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIGK 545
+AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIGK

Sbjct: 484

IAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIGK 543

Query: 546

GFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKV IIGLLVGAMLPYWFSAMTMKSVGSAA 605
GFAIGSAALVSLALFGAFVSRAG+ VDVLT PKV IGL+VGAMLPYWFSAMTMKSVGSAA

Sbjct: 544

GFAIGSAALVSLALFGAFVSRAGVTAVDVLT PKV FIGLIVGAMLPYWFSAMTMKSVGSAA 603

Query: 606

LKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFFFG 665
LKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPG LVMLTPLIVG FG

Sbjct: 604 LKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGALVMLTPLIVGILFG
663

Query: 666

VETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA KSLGPKGSEPHKAAVI 725
VETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAG S+HA++LGPKGS+PHKAAVI

Sbjct: 664

VETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGASKHARTLGPKGS DPHKAAVI 723

Query: 726 GDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

GDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFA+HGG+LFK F

Sbjct: 724 GDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFASHGGLLFKIF 768



>gi|7436046|pir|T14563 inorganic diphosphatase (EC 3.6.1.1) - beet

gi|485742|gb|AAA61609.1| pyrophosphatase [Beta vulgaris]

Length = 761

Score = 1202 bits (3109), Expect = 0.0

Identities = 646/765 (84%), Positives = 685/765 (89%), Gaps = 4/765 (0%)

Query: 6 LLPELWTEILVPICAVIGIAFSLFQWYVVS RVKLTSDLXXXXXXXXXXXXXXXXXXDY LIEE
65

++ +L TEI +P+CAVIG S +QW++VS+VK+++D DY LIEE

Sbjct: 1 MISDLATEIFIPVCAVIGY-ISCYQWFLVSKVKVSTD---RHVNNGGSAKNGFNDY LIEE 56

Query: 66

EEGVNDQSVVAKCAEIQT AISEGATSFLFTEYKYXXXXXXXXXXXXXXXXXXLGSVEGFSTDN 125

EEGVNDQ+VWAKCAEIQ AISEGATSFLFTEY+Y LGSVEGFST++

Sbjct: 57

EEGVNDQNVVAKCAEIQNAISEGATSFLFTEYQYVGVMCAFAVLIFVFLGSVEGFSTES 116

Query: 126

KPCTYDTRTCKPALATAAFSTIAFVLGAVTSVL SGFLGMKIATYANARTTLEARKGVGK 185

+PCTY + CKPALATA FST++F+LGA+TSV+SGFLGMKIAT ANARTTLEARKGVGK

Sbjct: 117

QPCTYSPLKKCKPALATALFSTVSFLLGAITSVVS GFLGMKIATDANARTTLEARKGVGK 176

Query: 186

AFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMALFG 245

AFI+AFRSGAVMGFLLAA+GLLVLYI IN+ K+YYGDDWEGLFEAITGYGLGGSSMALFG

Sbjct: 177

AFIIAFRSGAVMGFLLAANGLLVLYIAINLLKLYYGDDWEGLFEAITGYGLGGSSMALFG 236

Query: 246

RVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE 305

RVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE

Sbjct: 237

RVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE 296

Query: 306 ASCAALVVASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEIEPAL
365

ASCAALVVASISSFGINH+FTAMCYPLLISSMGI+VCL+TTLFATDFFEIK VKEIEPAL

Sbjct: 297 ASCAALVVASISSFGINHEFTAMCYPLLISSMGIIVCLVTTLFATDFFEIKAVKEIEPAL
356

Query: 366 KNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGLIIGFV
425

K QLIISTV+MTVGIAI++W+ LP+SFTIFNFGTQKV NWQLFLCVCVGLWAGLIIGFV
Sbjct: 357 KKQLIISTVLMTVGIAIITWIALPSSFTIFNFGTQKVHNWQLFLCVCVGLWAGLIIGFV
416

Query: 426

TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXMYG 485
TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK MYG
Sbjct: 417 TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAVSIFVSFSFAAMYG
476

Query: 486

VAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIGK 545
VAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIGK
Sbjct: 477
VAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIGK 536

Query: 546

GFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKV IIGLLVGAMLPYWFSAMTMKSVGSAA 605
GFAIGSAALVSLALFGAFVSRA I TVDVLT PKV IGL+VGAMLPYWFSAMTMKSVGSAA
Sbjct: 537
GFAIGSAALVSLALFGAFVSRAAISTVDVLT PKV FIGLIVGAMLPYWFSAMTMKSVGSAA 596

Query: 606

LKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFFG 665
LKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPG LVMLTPLIVG FFG
Sbjct: 597 LKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGALVMLTPLIVGFFG
656

Query: 666

VETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHKAAVI 725
VETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAG SEHA+SLGPKGSEPHKAAVI
Sbjct: 657
VETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGASEHARSLGPKGSEPHKAAVI 716

Query: 726 GDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

GDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGG+LFK F
Sbjct: 717 GDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGLLFKLF 761

☐ >gi|2129948|pir||S61424 inorganic diphosphatase (EC 3.6.1.1) (clone TVP31) - common tobacco
Length = 766

Score = 1172 bits (3032), Expect = 0.0
Identities = 639/770 (82%), Positives = 684/770 (88%), Gaps = 4/770 (0%)

Query: 1
MVAPALLPELWTEILVPICAVIGIAFSLFQWYVVS RVKLTSDLXXXXXXXXXXXXXXXXXXD 60
M AP +L +L TEIL+P+CAV+GIAFSLFQW++VS+V L++D +
Sbjct: 1 MGAP-ILSDLGTEILIPVCAVVGIAFSLFQWFLVSKVTLSAD---KSSGAADDKNGYAAE 56

Query: 61
YLIEEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXXXLGSVEG 120
LIEEEEG+ND +VV KCAEIQ AISEGATSFLFTEY+Y LGSVEG
Sbjct: 57 SLIEEEEGINDHNVVQKCAEIQNAISEGATSFLFTEYQYVGVMVAFAILIFLGLSVEG 116

Query: 121
FSTDNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEAR 180
FST N+PCTYD+T+TCKPALATA FST++F+LGAVTSV+SGFLGMKIATYANARTTLEAR
Sbjct: 117
FSTKNQPCTYDSTKTCKPALATAVFSTVSFLLGAVTSVSGFLGMKIATYANARTTLEAR 176

Query: 181
KGVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS 240
KGVGKAFIVAFRSGAVMGFLLAA+GLLVLYITI +FK+YYGDDWEGLFEAITGYGLGGSS
Sbjct: 177
KGVGKAFIVAFRSGAVMGFLLAANGLLVLYITILLFKLYYGDDWEGLFEAITGYGLGGSS 236

Query: 241

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF 300

MALFGRV GGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF

Sbjct: 237

MALFGRVAGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF 296

Query: 301 GSYAEASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKE
360

GSYAE+SCAALVVASISSFG+NH+FTAM YPLL+SS+GILVCL+TTLFATDFFE+K VKE

Sbjct: 297

GSYAESSCAALVVASISSFGVNHEFTAMLYPLLVS SVGILVCLLTTLFATDFFE VKAVKE 356

Query: 361

IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGL 420

IEPALK QL+IST +MTVGIA+V+W+ LP+ FTIFNFG QK VK+WQLFLCV VGLWAGL

Sbjct: 357 IEPALKQQLVISTALMTVGIAVVTWIALPSIFTIFNFGAQKEVKSWQLFLCVGVGLWAGL
416

Query: 421

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXX 480

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 417 IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKS VIIPIFAIVSIFVSFSF
476

Query: 481

XXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT 540

M +AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT

Sbjct: 477

AAMGYIAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT 536

Query: 541

AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMKS 600

AAIGKGFAIGSAALVSLALFGAFVSRA I TVDVLTPKV IGL+VGAMLPYWFSAMTMKS

Sbjct: 537

AAIGKGFAIGSAALVSLALFGAFVSRAAISTVDVLT PKVFIGLIVGAMLPYWFSAMTMKS 596

Query: 601

VGSAALKMVVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV 660

VGSAALKMVVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMI PG LVMLTPLIV

Sbjct: 597

VGSAALKMVVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIAPGALVMLTPLIV 656

Query: 661

GFFFGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA KSLGPKGSEPH 720

G FGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA++LGPKGS+ H

Sbjct: 657

GILFGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHARTLGPKGSDAH 716

Query: 721 KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGG+LFK F

Sbjct: 717 KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGLLFKLF 766



>gi|1103712|emb|CAA58700.1| inorganic pyrophosphatase [Nicotiana tabacum]

Length = 766

Score = 1180 bits (3053), Expect = 0.0

Identities = 641/770 (83%), Positives = 686/770 (89%), Gaps = 4/770 (0%)

Query: 1

MVAPALLPELWTEILVPICAVIGIAFSLFQWYVVS RVKLTSDLXXXXXXXXXXXXXXXXXXD 60

M AP +L +L TEIL+P+CAV+GIAFSLFQW++VS+V L++D +

Sbjct: 1 MGAP-ILSDLGTEILIPVCAVVGIAFSLFQWFLVSKVTL SAD---KSSGAADDKNGYAAE 56

Query: 61

YLIEEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXX LGSVEG 120

LIEEEEG+ND +VV KCAEIQ AISEGATSFLFTEY+Y LGSVEG

Sbjct: 57 SLIEEEEGINDHNVVQKCAEIQNAISEGATSFLFTEYQYVGVMVAFAILIFL LGSVEG

116

Query: 121

FSTDNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLGFLGMKIATYANARTTLEAR 180

FST N+PCTYD+T+TCKPALATA FST++F+LGAVTSV+SGFLGMKIATYANARTTLEAR

Sbjct: 117

FSTKNQPCTYDSTKTCKPALATAVFSTVSFLLGAVTSVWSGFLGMKIATYANARTTLEAR 176

Query: 181

KGVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS 240

KGVGKAFIVAFRSGAVMGFLLAA+GLLVLYITI +FK+YYGDDWEGLFEAITGYGLGGSS

Sbjct: 177

KGVGKAFIVAFRSGAVMGFLLAANGLLVLYITILLFKLYYGDDWEGLFEAITGYGLGGSS 236

Query: 241

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF 300

MALFGRV GGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF

Sbjct: 237

MALFGRVAGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF 296

Query: 301 GSYAEASCAALVVASISSFGINHFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKE
360

GSYAE+SCAALVVASISSFG+NH+FTAM YPLL+SS+GILVCL+TTLFATDFFE+K VKE

Sbjct: 297

GSYAESSCAALVVASISSFGVNHEFTAMLYPLLSSVGILVCLLTTLFATDFFEVKAVKE 356

Query: 361

IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVKNWQLFLCVCVGLWAGL 420

IEPALK QL+IST +MTVGIA+V+W+ LP+ FTIFNFG QK VK+WQLFLCV VGLWAGL

Sbjct: 357 IEPALKQQLVISTALMTVGIAVVTWIALPSIFTIFNFGAQKEVKSQWQLFLCVGVGLWAGL
416

Query: 421

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXX 480

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 417 IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSIIPIFAIVSIFVSFSF
476

Query: 481

XXMYGVAVALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT 540

MYG+AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT

Sbjct: 477

AAMYGIAVALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT 536

Query: 541

AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIIGLLVGAMLPYWFSAMTMKS 600

AAIGKGFAIGSAALVSLALFGAFVSRA I TVDVLT PKV IGLLVGAMLPYWFSAMTMKS

Sbjct: 537

AAIGKGFAIGSAALVSLALFGAFVSRAAISTVDVLT PKVFIGLLVGAMLPYWFSAMTMKS 596

Query: 601

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV 660

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMI PG LVMLTPLIV

Sbjct: 597

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIAPGALVMLTPLIV 656

Query: 661

GFFFGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA KSLGPKGSEPH 720

G FGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA++LGPKGS+ H

Sbjct: 657

GILFGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHARTLGPKGSDAH 716

Query: 721 KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

KAAVIGDT+GDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGG+LFK F

Sbjct: 717 KAAVIGDTVGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGLLFLKF 766



>gi|7436041|pir||S72526 inorganic diphosphatase (EC 3.6.1.1), H⁺-translocating, vacuolar membrane (clone OVP1) - rice

gi|1747294|dbj|BAA08232.1| vacuolar H⁺-pyrophosphatase [Oryza sativa (japonica cultivar-group)]

Length = 771

Score = 1169 bits (3023), Expect = 0.0

Identities = 634/769 (82%), Positives = 675/769 (87%), Gaps = 3/769 (0%)

Query: 5 ALLPELWTEILVPICAVIGIAFSLFQWYVVSrvKLTSDLXXXXXXXXXXXXXXXXXX---DY
61

A+LP+L T++LVP AV+GIAF++ QW +VS+VK+T++ +Y

Sbjct: 3

AILPDLATQVLVPAAAVVGIAFAVWQWVLVSKVKMTAERRGGEGSPGAAAGKDGAASEY 62

Query: 62

LIEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXX LGSVEGF 121

LIEEEG+N+ +VV KC+EIQ AISEGATSFLFTEYKY LGSVEGF

Sbjct: 63 LIEEEGLNEHNVVEKCEIQHAISEGATSFLFTEYKYVGLFMGIFAVLIFLFLGSVEGF
122

Query: 122

STDNKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARK 181

ST ++PC Y R CKPALA A FST+AFVLGAVTS++SGFLGMKIATYANARTTLEARK

Sbjct: 123

STKSQPCHYSKDRMCKPALANAIFSTVAFVLGAVTSLVSGFLGMKIATYANARTTLEARK 182

Query: 182

GVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSM 241

GVGKAFI AFRSGAVMGFLLAASGL+VLYI IN+F IYYGDDWEGLFEAITGYGLGGSSM

Sbjct: 183

GVGKAFITAFRSGAVMGFLLAASGLVLYIAINLFGIYYGDDWEGLFEAITGYGLGGSSM 242

Query: 242

ALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG 301

ALFGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG

Sbjct: 243

ALFGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG 302

Query: 302 SYAEASCAALVVASISSFGINHDF TAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEI
361

SYAE+SCAALVVASISSFGINH+FT M YPLLISS+GI+ CLITTLFATDFFEIK V EI

Sbjct: 303 SYAESSCAALVVASISSFGINHEFTPMLYPLLISSVGIIACLITTLFATDFFEIKAVDEI 362

Query: 362

EPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGLI 421

EPALK QLIISTV+MTVGIA+VSW+GLP SFTIFNFG QK V NWQLFLCV VGLWAGLI

Sbjct: 363

EPALKKQLIISTVVM TVGIALVSWLGLPYSFTIFNFGAQKTVYNWQLFLCVAVGLWAGLI 422

Query: 422

IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXX 481

IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 423 IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIIPFAIAFSIFLSFSLA
482

Query: 482

XYMGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA 541

MYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA

Sbjct: 483

AMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA 542

Query: 542

AIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMKSV 601

AIGKGFAIGSAALVSLALFGAFVSRA I TVDVLTPKV IGL+VGAMLPYWFSAMTMKSV

Sbjct: 543

AIGKGFAIGSAALVSLALFGAFVSRAAISTVDVLT PKVFIGLIVGAMLPYWFSAMTMKSV 602

Query: 602

GSAALKMVEEVRRQFN TIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVG 661

GSAALKMVEEVRRQFN+IPGLMEGT KPDYATCVKISTDASIKEMIPPG LVML+PLIVG

Sbjct: 603

GSAALKMVEEVRRQFNSIPGLMEGTTKPDYATCVKISTDASIKEMIPPGALVMLSPLIVG 662

Query: 662

FFFGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA KSLGPKGSEPHK 721

FFGVETLSG+LAG+LVSGVQIAISASNTGGAWDNAKKYIEAG SEHA++LGPKGS+ HK

Sbjct: 663

IFFGVETLSG LLAGALVSGVQIAISASNTGGAWDNAKKYIEAGASEHARTLGPKGSDCHK 722

Query: 722 AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770
AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFK+F
Sbjct: 723 AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKWF 771

☐ >gj|31580801|gb|AAP55210.1| vacuolar proton-inorganic pyrophosphatase [Triticum aestivum]

Length = 762

Score = 1132 bits (2928), Expect = 0.0

Identities = 612/765 (80%), Positives = 664/765 (86%), Gaps = 5/765 (0%)

Query: 5 ALLPELWTEILVPICAVIGIAFSLFQWYVVS RVKLTSDLXXXXXXXXXXXXXXXXXXDYLIE
64

A+L EL TEIL+P+C V+GI F++ QW++VS+VK+T DYLIE

Sbjct: 2 AILGELGTEILIPVCGVVGIVFAVAQWFIVSKVKVTPGAASAAGGGKNGYG----DYLIE 57

Query: 65

EEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXX LGSVEGFSTD 124

EEEG+ND +VV KCAEIQTASEGATSFLFT Y+Y LGS+EGFST

Sbjct: 58

EEEGLNDHNVVVKCAEIQTASEGATSFLFTMYQYVGMFMVFAAVIFVFLGSIEGFSTK 117

Query: 125

NKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVL SGFLGMKIATYANARTTLEARKGVG 184

+PCTY +T TCKPAL TA FST +F+LGA+TS++SGFLGMKIATYANARTTLEARKGVG

Sbjct: 118 GQPCTY-

STGTCKPALYTALFSTASFLLGAITSLVSGFLGMKIATYANARTTLEARKGVG 176

Query: 185

KAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMALF 244

KAFI AFRSGAVMGFLL++SGL VLYITINVFK+YYGDDWEGLFE+ITGYGLGGSSMALF

Sbjct: 177

KAFITAFRSGAVMGFLLSSSGLGVLYITINVFKMYYGDDWEGLFESITGYGLGGSSMALF 236

Query: 245

GRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYA 304

GRVGGGIYTKAADVGADLVGK+ERNIPED PRNPAVIADNVGDNVGDIAGMGSDLFGSYA

Sbjct: 237

GRVGGGIYTKAADVGADLVGKVERNIPEDGPRNPAVIADNVGDNVGDIAGMGSDLFGSYA 296

Query: 305 EASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEIEPA

364

E+SCAALVVASISSFGINHDFTAMCYPLL+SS+GI+VCL+TTLFATDFFEIK EIEPA

Sbjct: 297 ESSCAALVVASISSFGINHDFTAMCYPLLVS SVGIIVCLLTTLFATDFFEIKAASEIEPA

356

Query: 365 LKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGLIIGF

424

LK QLII T +MT+G+A+++W+ LP FTIFNFG QK V NW LF CV VGLWAGLIIGF

Sbjct: 357 LKKQLIIFTALMTIGVAVINWLALPAKFTIFNFGAQKDVSNWGLFFCVAVGLWAGLIIGF

416

Query: 425

VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXXMY 484

VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK MY

Sbjct: 417 VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIIPFAIAVSIYVSFSIAAMY

476

Query: 485

GVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIG 544

G+A+AALGMLST ATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIG

Sbjct: 477

GIAMAALGMLSTTATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIG 536

Query: 545

KGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMKSVGSA 604

KGFAIGSAALVSLALFGAFVSRAG+ VDL+PKV IGL+VGAMLPYWFSAMT + SA

Sbjct: 537

KGFAIGSAALVSLALFGAFVSRAGVKVVDVLS PKVFIGLIVGAMLPYWFSAMTRRVCESA 596

Query: 605

ALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFF 664

ALKMVE+VRRQFNTIPGLM+GTAKPDYATCVKISTDASI+EMIPPG LVMLTPLIVG F

Sbjct: 597

ALKMVEKVRQFNTIPGLMKGTAKPDYATCVKISTDASIREMIPPGALVMLTPLIVGTLF 656

Query: 665

GVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAHSLGPKGSEPHKAAV 724

GVETLSGVLAG+LVSGVQIAISASNTGGAWDNAKKYIEAG SEHA+SLGPKGS+ HKAAV

Sbjct: 657

GVETLSGVLAGALVSGVQIAISASNTGGAWDNAKKYIEAGNSEHARSLGPKGSDCHKAAV 716

Query: 725 IGDITGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKY 769

IGDITGDPLKDTSGPSLNILIKLMAVESLVFAPFFAT+GG+LFKY

Sbjct: 717 IGDITGDPLKDTSGPSLNILIKLMAVESLVFAPFFATYGGVLFKY 761



>gi|7739779|gb|AAF69010.1| H⁺-pyrophosphatase [Vitis vinifera]

Length = 759

Score = 1109 bits (2868), Expect = 0.0

Identities = 601/765 (78%), Positives = 665/765 (86%), Gaps = 10/765 (1%)

Query: 5 ALLPELWTEILVPICAVIGIAFSLFQWYVVS RVKLTSDLXXXXXXXXXXXXXXXXX DYLIE

64

++ + +T++L+P+ A++GI F+L QW +VS+VK+++D D LIE

Sbjct: 2 GVMGDAFTQLLIPVAALVGIGFALLQWLLVSKVKVSAD-----SDLNNGYS DRLIE 52

Query: 65 EEE-

GVNDQSVWAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXXLGSVEGFST 123

EEE G++ + V AKCAEIQ AIS GATSFLFTEY+Y LGSV+GFST

Sbjct: 53 EEEEGIDHEDVAAKCAEIQNAISVGATSFLFTEYRYLSIFMGVFGAIFLFLGSVKGFST

112

Query: 124

DNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGV 183

++PCTY+T CKPALA A FSTIAF+LGA+TSV SGFLGMKIATYANARTTLEARKGV

Sbjct: 113

KSEPCTYNTGSLCKPALANALFSTIAFLLGAMTSVFSGFLGMKIATYANARTTLEARKGV 172

Query: 184

GKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMAL 243

GKAFIVAFRSGAVMGFLLAASGLLVLY++I++F +YYGDDWEGL+E+ITGYGLGGSSMAL

Sbjct: 173

GKAFIVAFRSGAVMGFLLAASGLLVLYVSIHLFSLYYGDDWEGLYESITGYGLGGSSMAL 232

Query: 244

FGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSY 303

FGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSY

Sbjct: 233

FGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSY 292

Query: 304 AEASCAALVASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEIEP
363

AEASCAAL VASISSFGI+HD+TAM +PL+ISS+GI+VCL TTLFATDF EIK V EIEP

Sbjct: 293 AEASCAALFVASISSFGISHDYTAMSFPLIISVGIVVCLGTTTLFATDFVEIKNVSEIEP
352

Query: 364 ALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGLIIG
423

+LK QL+IST++MT GIA+VS+ LP+ FT+FNFG+ K VKNW LF CV +GLWAGL+IG

Sbjct: 353 SLKRQLLISTILMTAGIAVVSFFALPSEFTLFNFGSTKTVKNWHLFFCVSIGLWAGLVIG
412

Query: 424

FVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXM 483

++TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK M

Sbjct: 413 YITEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAIAIYVSFSMAAM
472

Query: 484

YGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAI 543
YG+AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSH+IR+RTDALDAAGNTTAAI

Sbjct: 473

YGIABAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHKIRQRTDALDAAGNTTAAI 532

Query: 544

GKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKV IIGLLVGAMLPYWFSAMTMKSVGS 603
GKGFAIGSAALVSLALFGAFVSRAGI TVDVLT PKV IGL+VGAMLPYWFSAMTMKSVGS

Sbjct: 533

GKGFAIGSAALVSLALFGAFVSRAGIETVDVLT PKV FIGLIVGAMLPYWFSAMTMKSVGS 592

Query: 604

AALKMVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFF 663
AALKMVEEVRQFNTIPGLMEG AKPDYATCVKISTDAS++EMIPPG LVMLTPLI G

Sbjct: 593

AALKMVEEVRQFNTIPGLMEGRAKPDYATCVKISTDASLREMIPPGALVMLTPLIAGTL 652

Query: 664

FGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA KSLGPKGSEPHKAA 723
FGVETL+GVLAGSLVSGVQ+AISASNTGGAWDNAKKYIEAG SEHA+SLGPKGS+PHKAA

Sbjct: 653

FGVETLAGVLAGSLVSGVQVAISASNTGGAWDNAKKYIEAGASEHARSLGPKGSDPHKAA 712

Query: 724 VIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFK 768

VIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFA HGG+LFK

Sbjct: 713 VIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFAAHGGLLFK 757



>[gi|7436042|pir|S72527](#) inorganic diphosphatase (EC 3.6.1.1), H⁺-translocating, vacuolar membrane (clone OVP2) - rice

[gi|1747296|dbj|BAA08233.1](#) vacuolar H⁺-pyrophosphatase [*Oryza sativa* (japonica cultivar-group)]

[gi|3298476|dbj|BAA31524.1](#) ovp2 [*Oryza sativa*]

[gi|24413986|dbj|BAC22237.1](#) putative inorganic pyrophosphatase [*Oryza sativa* (japonica

cultivar-group)]

Length = 767

Score = 1146 bits (2964), Expect = 0.0

Identities = 618/766 (80%), Positives = 667/766 (87%)

Query: 5 ALLPELWTEILVPICAVIGIAFSLFQWYVVS RVKLTSDLXXXXXXXXXXXXXXXXXXDYLIE
64

A+L L TE+ +P+ A +G+AF++ QW +V+RVK+ DYLIE

Sbjct: 2

AILSALGTEVFIPVAAAVGVAFAVAQWLLVARVKVNPAAAAAASGGSKNGGYGDYLIE 61

Query: 65

EEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXXLGSVEGFSTD 124

EEEG+ND +VV KC EIQTASEGATSFLFTEY+Y LGSVEGFST

Sbjct: 62 EEGLNDHNWVKCHEIQTASEGATSFLFTEYQYVGIFMSIFAVVIFLFLGSVEGFSTK
121

Query: 125

NKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLGFLGMKIATYANARTTLEARKGVG 184

++PCTY + CKPAL A FST +F+LGA+TS++SG+LGMKIAT+ANARTTLEARKGVG

Sbjct: 122

SQPCTYSKDKYCKPALFNALFSTASFLLGAITSLVSGYLGMIATFANARTTLEARKGVG 181

Query: 185

KAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMALF 244

KAFI+AFRSGAVMGFLLA+SGL+VLYI INVFK+YYGDDWEGLFE+ITGYGLGGSSMALF

Sbjct: 182

KAFIIAFRSGAVMGFLLASSGLVVLIAINVFKLYYGDDWEGLFESITGYGLGGSSMALF 241

Query: 245

GRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYA 304

GRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYA

Sbjct: 242

GRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYA 301

Query: 305 EASCAALVVASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEIEPA
364

E+SCAALVVASISSFGINHDT MCYPLL+SS+GI+VCLITTLFATDFFEIK VKEIEPA

Sbjct: 302 ESSCAALVVASISSFGINHDTGMCYPLLVS SVGIIVCLITTLFATDFFEIKAVKEIEPA
361

Query: 365 LKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVKNWQLFLCVCVGLWAGLIIGF
424

LK QLIIST +MTVGIAI+SW+ LP FTIFNFG QK V NW LF CV +GLWAGLIIGF

Sbjct: 362 LKKQLIISTALMTVGIAIISWLALPAKFTIFNFGAQKEVTNWGLFFCVAIGLWAGLIIGF
421

Query: 425

VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXXMY 484

VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK MY

Sbjct: 422 VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAVSIYVSFSIAAMY
481

Query: 485

GVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIG 544

G+AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIG

Sbjct: 482

GIAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIG 541

Query: 545

KGFAIGSAALVSLALFGAFVSRAGIHTVDLTPKVIIGLLVGAMLPYWFSAMTMKSVGSA 604

KGFAIGSAALVSLALFGAFVSRAG+ VDL+PKV IGL+VGAMLPYWFSAMTMKSVGSA

Sbjct: 542

KGFAIGSAALVSLALFGAFVSRAGVKVVDVLS PKVFIGLIVGAMLPYWFSAMTMKSVGSA 601

Query: 605

ALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFF 664

ALKMVEEVRRQFN+IPGLMEGT KPDYATCVKISTDASIKEMIPPG LVMLTPLIVG F

Sbjct: 602

ALKMVEEVRRQFNSIPGLMEGTGKPDYATCVKISTDASIKEMIPPGALVMLTPLIVGTLF 661

Query: 665

GVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA~~SLGPKGSEPHKAAV~~ 724

GVETLSGVLAG+LVSGVQIAISASNTGGAWDNAKKYIEAG SEHA++LGPKGS+ HKAAV


Sbjct: 662

GVETLSGVLAGALVSGVQIAISASNTGGAWDNAKKYIEAGASEHARTLGPKGSDCHKAAV 721

Query: 725 IGD~~TIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF~~ 770

IGD~~TIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGG~~+LFK+F

Sbjct: 722 IGD~~TIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGG~~LLFKWF 767

 [>gi|30027157|gb|AAP06752.1](#) vacuolar proton-inorganic pyrophosphatase [*Hordeum brevisubulatum*]

Length = 773

Score = 1166 bits (3016), Expect = 0.0

Identities = 634/772 (82%), Positives = 676/772 (87%), Gaps = 2/772 (0%)

Query: 1 MVAPALLPELWTEILVPICAVIGIAFSLFQWYVSRVKLTSD--LXXXXXXXXXXXXXXXXX
58

+VA A+LPEL T+++VP+ A +GIAF++ QW++VS+VK+ +

Sbjct: 2

VVAAAILPELATQLVVPVAAAVGIAFAVLQWFLVSKVKVAPERRGEGSGSAGAGGGKDGA 61

Query: 59

XDYLIEEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXXLGSV 118

+YLIEEEEG+ND +VV KCAEIQTASEGATSFLFTEYKY LGS+

Sbjct: 62 SEYLIEEEEG~~LNDHNVVLKCAEIQTASEGATSFLFTEYKYAGGFMTVFAVLIFVFLGSI~~
121

Query: 119

EGFSTDNKPCTYD~~TTRTCKPALATAAFSTIAFVLGAVTSVL~~SGFLGMKIATYANARTTLE 178

EGFST ++PC Y +TCKPALA AAFSTIAFVLGAVTS++SGFLGMKIATYANARTTLE

Sbjct: 122

EGFSTKSQ~~PCHYSVGKTCKPALANA~~AFSTIAFVLGAVTSVL~~SGFLGMKIATYANARTTLE~~ 181

Query: 179

ARKGVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGG 238

ARKGVGKAFIVAFRSGAVMGFLLAASGL VLY+ IN+F +YYGDDWEGLFEAITGYGLGG

Sbjct: 182

ARKGVGKAFIVAFRSGAVMGFLLAASGLFVLYVAINLFGLYYGDDWEGLFEAITGYGLGG 241

Query: 239

SSMALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSD 298

SSMALFGRVGGGIYTK ADVGADLVGK ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSD

Sbjct: 242

SSMALFGRVGGGIYTKTADVADLVGKEERNIPEDDPRNPAVIADNVGDNVGDIAGMGSD 301

Query: 299 LFGSYAEASCAALVVASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLV
358

LFGSYAE+SCAALVVASISSFGINH+FT M YPLLISS+GI+ CLITTLFATDFFE+K V

Sbjct: 302 LFGSYAESSCAALVVASISSFGINHEFTPMMPYLLIISVGIACLITTLFATDFFEVEK
361

Query: 359

KEIEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVKNWQLFLCVCVGLWA 418

+IEPALK QLIIST +MTVGIA+VSW+GLP +FTIFNFG QK V +WQLFLCV VGLWA

Sbjct: 362

DQIEPALKKQLIISTAVMTVGIALVSWLGLPYTFTIFNFGAQKTVHSWQLFLCVAVGLWA 421

Query: 419

GLIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXX 478

GL+IGF+TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 422 GLVIGFITEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAFSIFLSF
481

Query: 479

XXXXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGN 538

MYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGN

Sbjct: 482

SLAAMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGN 541

Query: 539

TTAAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTM 598

TTAAIGKGFAIGSAALVSLALFGAFVSRAGI TVDVLTP V IGLLVGAMLPYWFSAMTM

Sbjct: 542

TTAAIGKGFAIGSAALVSLALFGAFVSRAGITTVDVLT PNVFIGLLVGAMLPYWFSAMTM 601

Query: 599

KSVGSAALKMVVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPL 658

KSVGSAALKMVVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDAS KEMIPPG LVMLTPL

Sbjct: 602

KSVGSAALKMVVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASTKEMIPPGALVMLTPL 661

Query: 659

IVGFFFGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSE 718

IVG FFGVETLSGVLG+LVSGVQIAISASNTGGAWDNAKKYIEAG SEHAKSLGPKGS+

Sbjct: 662

IVGTFFGVETLSGVLGALVSGVQIAISASNTGGAWDNAKKYIEAGASEHAKSLGPKGSD 721

Query: 719 PHKAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

HKAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFAT+GGILFKY

Sbjct: 722 CHKAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATYGGILFKYL 773



>gj|18086404|gb|AAL57660.1| At1g15690/F7H2_3 [Arabidopsis thaliana]

Length = 770

Score = 1315 bits (3402), Expect = 0.0

Identities = 717/770 (93%), Positives = 718/770 (93%)

Query: 1

MVAPALLPELWTEILVPICAVIGIAFSLFQWYVVS RVKLTSDLXXXXXXXXXXXXXXXXXXD 60

MVAPALLPELWTEILVPICAVIGIAFSLFQWYVVS RVKLTSDL D

Sbjct: 1

MVAPALLPELWTEILVPICAVIGIAFSLFQWYVVS RVKLTSDLGASSSGGANNGKNGYGD 60

Query: 61

YLIEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXX LGSVEG 120

YLIEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKY LGSVEG

Sbjct: 61 YLIEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYVGVFMIFFAVIFVFLGSVEG
120

Query: 121

FSTDNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEAR 180

FSTDNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEAR

Sbjct: 121

FSTDNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEAR 180

Query: 181

KGVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS 240

KGVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS

Sbjct: 181

KGVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS 240

Query: 241

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF 300

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF

Sbjct: 241

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF 300

Query: 301 GSYAEASCAALVVASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKE
360

GSYAEASCAALVVASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKE

Sbjct: 301 GSYAEASCAALVVASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKE
360

Query: 361

IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKWQFLCVCVGLWAGL 420

IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKWQFLCVCVGLWAGL

Sbjct: 361 IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKWQFLCVCVGLWAGL
420

Query: 421

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXX 480

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 421 IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAISIFVSFSF
480

Query: 481

XXMYGVAVALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT 540

MYGVAVALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT

Sbjct: 481

AAMYGVAVALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT 540

Query: 541

AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMKS 600

AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMKS

Sbjct: 541

AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMKS 600

Query: 601

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV 660

VGSAALKMVEEVRRQFNTIPGLM+GTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV

Sbjct: 601

VGSAALKMVEEVRRQFNTIPGLMKGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV 660

Query: 661

GFFFGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA KSLGPKGSEPH 720

GFFFGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA KSLGPKGSEPH

Sbjct: 661

GFFFGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA KSLGPKGSEPH 720

Query: 721 KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF

Sbjct: 721 KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

□ >gi|542059|pir|S42893 inorganic diphosphatase (EC 3.6.1.1) - common tobacco
gi|457744|emb|CAA54869.1| inorganic pyrophosphatase [Nicotiana tabacum]

Length = 764

Score = 1197 bits (3096), Expect = 0.0

Identities = 644/769 (83%), Positives = 682/769 (88%), Gaps = 5/769 (0%)

Query: 2 VAPALLPELWTEILVPICAVIGIAFSLFQWYVVS RVKLTSDLXXXXXXXXXXXXXXXXXXDY
61

+ ALLP+L T+I++P+CAVIGI FS FQWY+VSRVK++S+ D

Sbjct: 1

MGSALLPDLGTQIVIPVCAVIGIVFSSFQWYLVSRVKVSSEHGATSPSSNKNKNGYGDC 60

Query: 62

LIEEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXXXLGSVEGF 121

LIEEEEG+ND +VAKCA+IQ AISEGATSFLFTEY+Y LGSVEGF

Sbjct: 61 LIEEEEGINDHNVVAKCADIQNAISEGATSFLFTEYQYVGIFMIAFAILIFLGLSVEGF
120

Query: 122

STDNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARK 181

ST ++PCTY+ +CKPALATA FST++F+LGA+TSV+SGFLGMKIATYANARTTLEARK

Sbjct: 121 STSSQPCTYNKEKRCKPALATAIFSTVSFLLGAITSVISGFLGMKIATYANARTTLEARK
180

Query: 182

GVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSM 241

GVGKA +V VMGFLLAA+GLLVLYI IN+FK+YYGDDWEGLFEAITGYGLGGSSM

Sbjct: 181 GVGKACLQ-----VMGFLLAANGLLVLYIAINLFKLYYGDDWEGLFEAITGYGLGGSSM
235

Query: 242

ALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG 301

ALFGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG

Sbjct: 236

ALFGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG 295

Query: 302 SYAEASCAALVVASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEI
361

SYAE+SCAALVVASISSFGI+HDFTAMCYPLLISSMGILVCLITTLFATDFFEIK VKEI

Sbjct: 296 SYAESSCAALVVASISSFGIDHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKAVKEI
355

Query: 362

EPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKWQFLCVCVGLWAGLI 421

EPALKNQLIIST IMTVGIAIV+W LP+SFTIFNFGTQKVVKWQFLCV VGLWAGLI

Sbjct: 356 EPALKNQLIISTAIMTVGIAIVTWTCLPSSFTIFNFGTQKVVKWQFLCVAVGLWAGLI
415

Query: 422

IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXXX 481

IGFVTEYYTSNAYSPVQDVADSC TGAATNVIFGLALGYK

Sbjct: 416 IGFVTEYYTSNAYSPVQDVADSCSTGAATNVIFGLALGYKSVIPIFAIAIAFVSFTFA
475

Query: 482

XMYGVAVALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA 541

MYG+AVAAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA

Sbjct: 476

AMYGIAVALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA 535

Query: 542

AIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMKSV 601

AIGKGFAIGSAALVSLALFGAFVSRAGI TVDVLT+V IGL+VGAMLPYWFSAMTMKSV

Sbjct: 536

AIGKGFAIGSAALVSLALFGAFVSRAGISTVDVLT PQVFIGLIVGAMLPYWFSAMTMKSV 595

Query: 602

GSAALKMVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVG 661

GSAALKMVEEVRQFNTIPGLMEG AKPDYATCVKISTDASIKEMIPPG LVMLTPLIVG

Sbjct: 596

GSAALKMVEEVRQFNTIPGLMEGLAKPDYATCVKISTDASIKEMIPPGALVMLTPLIVG 655

Query: 662

FFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA⁺SLGPKGSEPHK 721

FFGVETLSGVLAG+LVSGVQIAISASNTGGAWDNAKKYIEAG SEHA⁺⁺LGPKGSEPHK

Sbjct: 656

IFFGVETLSGVLAGALVSGVQIAISASNTGGAWDNAKKYIEAGASEHARTLGPKGSEPHK 715

Query: 722 AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFK F

Sbjct: 716 AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKIF 764

☐ >gi|25901033|dbj|BAC41250.1| vacuolar proton-inorganic pyrophosphatase [Pyrus communis]

Length = 767

Score = 1188 bits (3073), Expect = 0.0

Identities = 643/765 (84%), Positives = 681/765 (89%), Gaps = 1/765 (0%)

Query: 6 LLPELWTEILVPICAVIGIAFSLFQWYVVS^{RV}KLTS^{DL}XXXXXXXXXXXXXXXXXXXXDY^{LIEE}

65

LL L TEI^{++P} AV⁺GI FSL QW^{++VS} VK⁺T + DY^{LIEE}

Sbjct: 4 LLSTLATEIVIPVA^{AVV}GIVFSLVQWFLVSLVKVTPE-RNAPPSGPN^{SNK}NGCNDY^{LIEE}

62

Query: 66

EEGVNDQSVVAKCAEIQT^AISEGATSFLFTEYKYXXXXXXXXXXXXXXXXXXLGSVEGFSTDN 125

EEG⁺NDQ⁺VV KCAEIQ AISEG⁺TSFLFT Y⁺Y LGSVEGFST +

Sbjct: 63

EEGLNDQNVVWKCAEIQNAISEGSTSFLFTMYQYGVGVFMVVF^{AILIFL}FLGSVEGFSTKS 122

Query: 126

KPCTYD^{TTR}TCKPALATAAFSTIAFVLGAVTSVL^{SGFL}GMKIATYANARTTLEARKGVGK 185

+PCTYD +TCKPALATA FST⁺AFVLG +TSVL^{SGFL}GMKIATYANARTTLEARKGVGK

Sbjct: 123

QPCTYDAAKTCKPALATAIFSTVAFVLGGITSVL^{SGFL}GMKIATYANARTTLEARKGVGK 182

Query: 186

AFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMALFG 245

AFI AFRSGAVMGFLLAA+GLLVL+ITIN+FK+YYGDDWEGLFE+ITGYGLGGSSMALFG

Sbjct: 183

AFITAFRSGAVMGFLLAANGLLVLFITINLFLKLYYGDDWEGLFESITGYGLGGSSMALFG 242

Query: 246

RVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE 305

RVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE

Sbjct: 243

RVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE 302

Query: 306 ASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEIEPAL
365

+SCAALVVASISSFGINH+FT M YPLLISS+GI+VCLITTLFATDFFEIK VKEIEPAL

Sbjct: 303 SSCAALVVASISSFGINHEFTPMLYPLLISSVGIIVCLITTLFATDFFEIKAVKEIEPAL 362

Query: 366 KNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKWQWQLFLCVCVGLWAGLIIGFV
425

K QLIISTV+MT+GIAIVSW+ LP+SFTIFNFG QKVVKWQWQLFLCV VGLWAGLIIGFV

Sbjct: 363 KKQLIISTVIMTVGIAIVSWIALPSSFTIFNFGVQKVVKWQWQLFLCVAVGLWAGLIIGFV
422

Query: 426

TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXXXMYG 485

TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK MYG

Sbjct: 423 TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAVSIYVSFSAAMYG
482

Query: 486

VAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIGK 545

+AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIGK

Sbjct: 483

IAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIGK 542

Query: 546

GFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKV IIGLLVGAMLPYWFSAMTMKSVGSAA 605

GFAIGSAALVSLALFGAFVSRA I TVDVLTPKV IGL+VGAMLPYWFSAMTMKSVGSAA

Sbjct: 543

GFAIGSAALVSLALFGAFVSRAAISTVDVLT PKV FIGLIVGAMLPYWFSAMTMKSVGSAA 602

Query: 606

LKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFFFG 665

LKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPG LV+LTPLIVG FFG

Sbjct: 603 LKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGALVILTPLIVGTFFG
662

Query: 666

VETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA KSLGPKGSEPHKAAVI 725

VETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAG SEHA++LGPKGS+PHKAAVI

Sbjct: 663

VETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGASEHARTLGPKGSDPHKAAVI 722

Query: 726 GDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

GDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGG+LFK F

Sbjct: 723 GDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGLLFKIF 767

☐ >gi|22532391|gb|AAM97920.1| vacuolar proton-pumping PPase [Chenopodium rubrum]

gi|22532393|gb|AAM97921.1| vacuolar proton-pumping PPase [Chenopodium rubrum]

Length = 764

Score = 1179 bits (3049), Expect = 0.0

Identities = 638/765 (83%), Positives = 678/765 (88%), Gaps = 5/765 (0%)

Query: 6 LLPELWTEILVPICAVIGIAFSLFQWYVVS RVKLTSDLXXXXXXXXXXXXXXXXXXDYLIEE

65

LLP+L TEIL+P+CAVIGI FSL QWYVVS+VKL+ D + LIEE

Sbjct: 5 LLPDLGTEILIPVCAVIGIVFSLIQWYVVSQVKLSPD-----SGRSNNNKNKFSEN LIEE 59

Query: 66

EEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXX LGSVEGFSTDN 125

EEG+NDQSVVAKCAEIQ AISEG+TSFL+T Y+Y LGSVEGFST +

Sbjct: 60 EEGINDQSVVAKCAEIQNAISEGSTSFLYTMYYQYVGIFMIAFAVLIFVFLGSVEGFSTKS
119

Query: 126

KPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVGK 185

+ CTYD ++TCKPALATA FST++F+LGAVTS+ SGFLGMKIATYANARTTLEARKGVGK

Sbjct: 120

QECTYDKSKTCKPALATAIFSTVSFLLGAVTSLASGFLGMKIATYANARTTLEARKGVGK 179

Query: 186

AFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMALFG 245

AFIVAFRSGAVMGFLLAA+GLLVLYITI +FK+YYGDDWEGLFEAITGYGLGGSSMALFG

Sbjct: 180

AFIVAFRSGAVMGFLLAANGLLVLYITILLFKLYGDDWEGLFEAITGYGLGGSSMALFG 239

Query: 246

RVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE 305

RVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE

Sbjct: 240

RVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE 299

Query: 306 ASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEIEPAL
365

+SCAALVVASISSFGINH+ TA+ YPLLISS+GI++CLITTLFATDFFEIK VKEIEPAL

Sbjct: 300 SSCAALVVASISSFGINHELTAILYPLLISSVGIVICLITTLFATDFFEIKAVKEIEPAL 359

Query: 366 KNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVKNWQLFLCVCVGLWAGLIIGFV
425

K QL+IST +MTV +A++SWV LP+SFTIF+FG+Q+ VKNWQLFLCV VGLWAGLIIGFV

Sbjct: 360

KKQLVISTALMTVAVAVISWVALPSSFTIFDFGSQREVKNWQLFLCVAVGLWAGLIIGFV 419

Query: 426

TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXXMYG 485

TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK MYG
Sbjct: 420 TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAVSIFVSFSFAAMYG
479

Query: 486
VAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIGK 545
+AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIGK

Sbjct: 480
IAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIGK 539

Query: 546
GFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKV IIGLLVGAMLPYWFSAMTMKSVGSAA 605
GFAIGSAALVSLALFGAFVSRA I TVDVLT PKV IIGLLVGAMLPYWFSAMTMKSVGSAA

Sbjct: 540
GFAIGSAALVSLALFGAFVSRAAISTVDVLT PKV FIGLLVGAMLPYWFSAMTMKSVGSAA 599

Query: 606
LKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFFG 665
LKMVEEVRRQFN IPGLMEGTAKPDYA CVKISTDASIKEMIPPG LVMLTPLIVG FG

Sbjct: 600
LKMVEEVRRQFNEIPGLMEGTAKPDYANCVKISTDASIKEMIPPGALVMLTPLIVGTLFG 659

Query: 666
VETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA KSLGPKGSEPHKAAVI 725
VETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAG SEHA+ LGPKGS+ HKA A VI

Sbjct: 660
VETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGASEHARQLGPKGSDAHKAAVI 719

Query: 726 GDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770
GDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGG+LFK F
Sbjct: 720 GDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGLLFKIF 764

□ [>gi|7436047|pir|T14564](#) inorganic diphosphatase (EC 3.6.1.1), vacuolar - beet
[gi|485744|gb|AAA61610.1|](#) pyrophosphatase [Beta vulgaris]

Length = 765

Score = 1168 bits (3022), Expect = 0.0

Identities = 635/770 (82%), Positives = 677/770 (87%), Gaps = 6/770 (0%)

Query: 2 VAPALLPELWTEILVPICAVIGIAFSLFQWYVVS RVKLTSDLXXXXXXXXXXXXXXXXXXDY
61

+ ALLP+L TEI++P+CAVIGIAFSL QWY+V RVKL+ D D

Sbjct: 1 MGAALLPDLITEIIPVCAVIGIAFSLQWYIVLRVKLSPD-----STRNNNNKNGFSDS 55

Query: 62

LIEEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXX LGSVEGF 121

LIEEEEG+NDQSVVAKCAEIQ AISEGATSFLFTEY+Y LGSVEGF

Sbjct: 56 LIEEEEGVNDQSVVAKCAEIQNAISEGATSFLFTEYQYVGIFMVAFAVLIFLFLGSVEGF
115

Query: 122

STDNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLGSGFLGMKIATYANARTTLEARK 181

ST ++ CTYD TR CKPALATA FST+AF+LGA+TS+ SGF GMKIATYANARTTLEARK

Sbjct: 116

STSSQECTYDKTRRCKPALATAIFSTVAFLLGAITSLSGSGFFGMKIATYANARTTLEARK 175

Query: 182

GVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSM 241

GVGKAFIVAFRSGAVMGFLLAA+GLLVLYITI +FKIYYGDDWEGLFEAITGYGLGGSSM

Sbjct: 176

GVGKAFIVAFRSGAVMGFLLAANGLLVLYITILLFKIYYGDDWEGLFEAITGYGLGGSSM 235

Query: 242

ALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF- 300

ALFGRV GGIYTKAADVGADLVGK+ER+IPEDDPRNPAVIADNVGDNVGDIAG G +F

Sbjct: 236

ALFGRVAGGIYTKAADVGADLVGKVERDIPEDDPRNPAVIADNVGDNVGDIAGYGVLI FL 295

Query: 301 GSYAEASCAALVVASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKE
360

SYAE+SCAALVV SISSFGI+HD TAM YPLL+SS+GI+VCLITTLFATDFFEIK VKE

Sbjct: 296 DSYAESSCAALVVRSSISFGISHDLTAMMYPLLSSVGIIVCLITTLFATDFFEIKAVKE
355

Query: 361

IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVKNWQLFLCVCVGLWAGL 420

IEPALK QLIIST +MTVG+A++SW+ LPTSFTIF+FG+QK V+NWQLFLCV VGLWAGL

Sbjct: 356 IEPALKKQLIISTALMTVGVAVISWIALPTSFTIFDFGSQKEVQNWQLFLCVAVGLWAGL
415

Query: 421

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXX 480

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 416 IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAISIFVSFSF
475

Query: 481

XXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT 540

MYG+A+AALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT

Sbjct: 476

AAMYGIAMAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT 535

Query: 541

AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTTPKVIIIGLLVGAMLPYWFSAMTMKS 600

AAIGKGFAIGSAALVSLALFGAFVSRA I TVDVLTPKV IGL+VGAMLPYWFSAMTMKS

Sbjct: 536

AAIGKGFAIGSAALVSLALFGAFVSRASIQTVDVLTTPKVFIGLIVGAMLPYWFSAMTMKS 595

Query: 601

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV 660

VGSAALKMVEEV +QFNTIPGL+EGTAKPDYATCVKISTDASIKEMIPPG LVMLTPLIV

Sbjct: 596 VGSAALKMVEEVPKQFNTIPGLLEGTAKEPDYATCVKISTDASIKEMIPPGALVMLTPLIV
655

Query: 661

GFFFGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAHSLGPKGSEPH 720

G FFGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAG SEHA++LGPKGS+ H

Sbjct: 656

GTFFGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGASEHARTLGPKGSDAH 715

Query: 721 KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGG+LFKY

Sbjct: 716 KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGLLFKYL 765

☐ >gi|11527561|dbj|BAB18681.1| vacuolar proton-inorganic pyrophosphatase [Hordeum
vulgare subsp.

vulgare]

Length = 771

Score = 1157 bits (2994), Expect = 0.0

Identities = 632/769 (82%), Positives = 674/769 (87%), Gaps = 1/769 (0%)

Query: 1 MVAPALLPELWTEILVPICAVIGIAFSLFQWYVVS RVKLTSD-LXXXXXXXXXXXXXXXXXXXX

59

MVA A+LPEL T+++VP+ A +GIAF++ QW +VS+VK+ +

Sbjct: 1

MVAAAAILPELATQLVVPVAAAVGIAFAVLQWVLVSKVKVAPEPRAEGGSASAVGAKDGAT 60

Query: 60

DYLIEEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXXXLGSVE 119

+YLIEEEEG+ND +VV KCAEIQTASEG TSFLFTEYKY LGS+E

Sbjct: 61 EYLIEEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYAGGFMTIFAVLIFVFLGSIE

120

Query: 120

GFSTDNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLGFLGMKIATYANARTTLEA 179

GFST ++PC Y +TCKPALA AAFSTIAFVLGAVTS++SGFLGMKIATYANARTTLEA

Sbjct: 121

GFSTKSQPCHYSVGKTCKPALANAFAFSTIAFVLGAVTSVLGFLGMKIATYANARTTLEA 180

Query: 180

RKGVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGS 239

RKGVGKAFI AFRSGAVMGFLLAASGL VLY+ IN+F +YYGDDWEGLFEAITGYGLGGS

Sbjct: 181

RKGVGKAFITAFRSGAVMGFLLAASGLFVLYVAINLFGLYYGDDWEGLFEAITGYGLGGS 240

Query: 240

SMALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDL 299

SMALFGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDL

Sbjct: 241

SMALFGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDL 300

Query: 300 FGSYAEASCAALVVASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVK
359

FGSYAE+SCAALVVASISSFGINH+FT M YPLLISS+GI+ CLITTLFATDFFE+K V

Sbjct: 301 FGSYAESSCAALVVASISSFGINHFTPMYPLLISSVGIIACLITTLFATDFFEVEVD
360

Query: 360

EIEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKWQLFLCVCVGLWAG 419

+IEPALK QLIIST +MT+GIA+VSW+GLP +FTIFNFG QK V +WQLFLCV VGLWAG

Sbjct: 361

QIEPALKRQLIISTAVMTIGIALVSWLGLPYTFTIFNFGAQKTVHSWQLFLCVAVGLWAG 420

Query: 420

LIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXX 479

L+IGF+TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 421 LVIGFITEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAFSIFLSFS
480

Query: 480

XXXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNT 539

MYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNT

Sbjct: 481

LAAMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNT 540

Query: 540

TAAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTTPKVIIGLLVGAMLPYWFSAMTMK 599

TAAIGKGFAIGSAALVSLALFGAFVSRAGI TVDVLTP V IGLLVGAMLPYWFSAMTMK

Sbjct: 541

TAAIGKGFAIGSAALVSLALFGAFVSRAGITTVDVLTPNVFIGLLVGAMLPYWFSAMTMK 600

Query: 600

SVGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLI 659

SVGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPG LVMLTPLI

Sbjct: 601

SVGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGALVMLTPLI 660

Query: 660

VGFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAHSLGPKGSEP 719

VG FGVETLSGVLAG+LVSGVQIAISASNTGGAWDNAKKYIEAG SEHAHSLGPKGS+

Sbjct: 661

VGTFLGVETLSGVLAGALVSGVQIAISASNTGGAWDNAKKYIEAGASEHAHSLGPKGSDC 720

Query: 720 HKAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFK 768

HKAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFAT+GGILFK

Sbjct: 721 HKAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATYGGILFK 769



>gi|3402487|dbj|BAA32210.1| Vacuolar proton pyrophosphatase [Arabidopsis thaliana]

Length = 770

Score = 1311 bits (3392), Expect = 0.0

Identities = 717/770 (93%), Positives = 717/770 (93%)

Query: 1

MVAPALLPELWTEILVPICAVIGIAFSLFQWYVSRVKLTSDLXXXXXXXXXXXXXXXXXXD 60

MVAPALL ELWTEILVPICAVIGIAFSLFQWYVSRVKLTSDL D

Sbjct: 1

MVAPALLLELWTEILVPICAVIGIAFSLFQWYVSRVKLTSDLGASSSGGANNGKNGYGD 60

Query: 61

YLIEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXX LGSVEG 120

YLIEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKY LGSVEG

Sbjct: 61 YLIEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYVGVFMIFFAVIFVFLGSVEG
120

Query: 121

FSTDNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEAR 180

FSTDNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEAR

Sbjct: 121

FSTDNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEAR 180

Query: 181

KGVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS 240

KGVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS

Sbjct: 181

KGVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS 240

Query: 241

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF 300

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF

Sbjct: 241

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF 300

Query: 301 GSYAEASCAALVVASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKE
360

GSYAEASCAALVVASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKE

Sbjct: 301 GSYAEASCAALVVASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKE
360

Query: 361

IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGL 420

IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGL

Sbjct: 361 IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGL
420

Query: 421

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXX 480

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 421 IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIIPFAIAISIFVSFSF
480

Query: 481

XXMYGVAVALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT 540

MYGVAVALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT

Sbjct: 481

AAMYGVAVALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT 540

Query: 541

AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMKS 600

AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMKS

Sbjct: 541

AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMKS 600

Query: 601

VGSAALKMVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV 660

VGSAALKMVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV

Sbjct: 601

VGSAALKMVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV 660

Query: 661

GFFFGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPH 720

GFFFGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPH

Sbjct: 661

GFFFGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPH 720

Query: 721 KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF

Sbjct: 721 KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

□ >gj|45479863|gb|AAS66771.1| PPase [Hevea brasiliensis]
Length = 769

Score = 1207 bits (3122), Expect = 0.0
Identities = 651/766 (84%), Positives = 685/766 (89%)

Query: 5 ALLPELWTEILVPICAVIGIAFSLFQWYVVSrvKLTSDLXXXXXXXXXXXXXXXXXXDYLIE
64

A+L EL TEILVP+CAV+GI FSL QWY+VSRVKLT + D LIE

Sbjct: 4 AVLSELGTEILVPVCAVVGIVFSLIQWYLVSRVKLTPERQAPGSSPAGANKNGYNDCLIE
63

Query: 65
EEEGVNDQSVVAKCAEIQTaiseGATSFLFTEYKYXXXXXXXXXXXXXXXXXLGsVEGFSTD 124
EEEG+ND SVVAKCAEI+TAISEGATSFLFTEY+Y LGSVEGFST
Sbjct: 64 EEEGLNDHsvVAKCAEIRTAISEGATSFLFTEYQYVGVFMVAFailIFLFLGSVEGFSTK
123

Query: 125
NKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVG 184
++PCTYD +TCKPALATA FST++F+LGA TSV+SGFLGMKIATYANARTTLEARKGVG
Sbjct: 124
SQPCTYDKQKTCKPALATAIFSTVSFLLGAFTSVVSgFLGMKIATYANARTTLEARKGVG 183

Query: 185
KAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMALF 244
KAFI AFRSGAVMGFLLAA+GLLVLYI IN+FK+YYG+DWEGLFE+ITGYGLGGSSMALF
Sbjct: 184
KAFITAFRSGAVMGFLLAANGLLVLyIAINLFKLYYGEDWEGLFESITGYGLGGSSMALF 243

Query: 245
GRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYA 304
GRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYA
Sbjct: 244
GRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYA 303

Query: 305 EASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEIEPA
364

E+SCAALVV ISSFGINHDFTAM YPLLISS+GILVCLITTLFATDFFEIK VKEIEPA
Sbjct: 304 ESSCAALVVPISSFGINHDFTAMLYPLLISSVGILVCLITTLFATDFFEIKAVKEIEPA
363

Query: 365 LKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKWQLFLCVCVGLWAGLIIGF
424

LK QLIISTV+MTVGIAIV+W+GLP+SFTIFNFGTQKVVKWQLFLCV VGLWAGLIIGF
Sbjct: 364 LKKQLIISTVLMTVGIAIVTWIGLPSSFTIFNFGTQKVVKWQLFLCVAVGLWAGLIIGF
423

Query: 425
VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXXXXXXMY 484
VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK MY
Sbjct: 424 VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIIPFAIAIGIFVSFSFAAMY
483

Query: 485
GVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIG 544
G+AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIG
Sbjct: 484
GIAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIG 543

Query: 545
KGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMKSVGSA 604
KGFAIGSAALVSLALFGAFVSRA I TVDVLT PKV IGL+VGAMLPYWFSAMTMKSVGSA
Sbjct: 544
KGFAIGSAALVSLALFGAFVSRASISTVDVLT PKVFIGLIVGAMLPYWFSAMTMKSVGSA 603

Query: 605
ALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFF 664
ALKMVEEVRRQFNTIPGLMEG AKPDYATCVKISTDASIKEMIPPG LVMLTPLIVG FF
Sbjct: 604
ALKMVEEVRRQFNTIPGLMEGHAKPDYATCVKISTDASIKEMIPPGALVMLTPLIVGTFF 663

Query: 665

GVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA⁺SLGPKGSEPHKAAV 724
GVETLSGVLG+LVSGVQIAISASNTGGAWDNAKKYIEAG SEHA⁺⁺LGPKGS+PHKAAV

Sbjct: 664

GVETLSGVLGALVSGVQIAISASNTGGAWDNAKKYIEAGASEHARTLGPKGSDPHKAAV 723

Query: 725 IGD^TIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

IGD^TIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGG+LFK F

Sbjct: 724 IGD^TIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGLLFKMF 769

☐ >gi|2827755|sp|P21616|AVP3_PHAU Pyrophosphate-energized vacuolar membrane
proton pump

(Pyrophosphate-energized inorganic pyrophosphatase)

(H⁺-PPase) (Vacuolar H⁺-pyrophosphatase)

gi|7436048|pir||T10841 inorganic diphosphatase (EC 3.6.1.1) - mung bean

gi|951323|gb|AAC49175.1| pyrophosphatase

Length = 765

Score = 1171 bits (3030), Expect = 0.0

Identities = 638/769 (82%), Positives = 681/769 (88%), Gaps = 4/769 (0%)

Query: 2 VAPALLPELWTEILVPICAVIGIAFSLFQWYVVS^RVKL^TSDLXXXXXXXXXXXXXXXXXXXXY
61

+ A+LP+L TEIL+P+CAVIGIAF+LFQW +VS+VKL++ DY

Sbjct: 1 MGAAILPDLGTEILIPVCAVIGIAFALFQWLLVSKVKLSA--VRDASPNA^AAKNGYNDY 57

Query: 62

LIEEEEGVNDQSVVAKCAEIQT^AISEGATSFLFTEYKYXXXXXXXXXXXXXXXXX^LGSVEGF 121

LIEEEEG+ND +VV KCAEIQT^AISEGATSFLFTEYKY LGSVEGF

Sbjct: 58 LIEEEEGINDHN^VVKCAEIQT^AISEGATSFLFTEYKYVGIFMVAFAILFLGSVEGF
117

Query: 122

STDNKPCTYD^TTRTCKPALATAAFSTIAFVLGAVTSVL^SSGFLGMKIATYANARTTLEARK 181

ST + C+YD T+TCKPALATA FST++F+LG VTS++SGFLGMKIATYANARTTLEARK
Sbjct: 118
STSPQACSYDKTKTCKPALATAIFSTVSFLLGGVTSLSVSGFLGMKIATYANARTTLEARK 177

Query: 182
GVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSM 241
GVGKAFI AFRSGAVMGFLLAA+GLLVLYI IN+FKIYYGDDW GLFEAITGYGLGGSSM
Sbjct: 178
GVGKAFITAFRSGAVMGFLLAANGLLVLYIAINLFKIYYGDDWGGLFEAITGYGLGGSSM 237

Query: 242
ALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG 301
ALFGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG
Sbjct: 238
ALFGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG 297

Query: 302 SYAEASCAALVVASISSFGINHDF TAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEI
361
SYAE+SCAALVVASISSFG+NH+ TAM YPL++SS+GILVCL+TTLFATDFFEIK VKEI
Sbjct: 298 SYAESSCAALVVASISSFGLNHELTAMLYPLIVSSVGILVCLLTTLFATDFFEIKAVKEI
357

Query: 362
EPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGLI 421
EPALK QL+ISTV+MT+G+A+VS+V LPTSFTIFNFG QK VK+WQLFLCV VGLWAGLI
Sbjct: 358
EPALKKQLVISTVLMTIGVAVVSFVALPTSFTIFNFGVQKDVKSWQLFLCVAVGLWAGLI 417

Query: 422
IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXXX 481
IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK
Sbjct: 418 IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAISIFVSFTFA
477

Query: 482
XMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA 541
MYG+AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA

Sbjct: 478

AMYGIAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA 537

Query: 542

AIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMKSV 601

AIGKGFAIGSAALVSLALFGAFVSRA I TVDVLT PKV IGL+VGAMLPYWFSAMTMKSV

Sbjct: 538 AIGKGFAIGSAALVSLALFGAFVSRASITTVDVLT PKVFIGLIVGAMLPYWFSAMTMKSV
597

Query: 602

GSAALKMVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVG 661

GSAALKMVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPG LVMLTPL+VG

Sbjct: 598

GSAALKMVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGALVMLTPLVVG 657

Query: 662

FFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHK 721

FGVETLSGVLAGSLVSGVQIAISASNT GAWDNAKKYIEAG SEHA+SLGPKGS+ HK

Sbjct: 658 ILFGVETLSGVLAGSLVSGVQIAISASNT-

GAWDNAKKYIEAGASEHARSLGPKGSDCHK 716

Query: 722 AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGG+LFK F

Sbjct: 717 AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGLLFKIF 765

□ >gi|41023649|emb|CAF18416.1| proton translocating pyrophosphatase [Oryza sativa]

Length = 762

Score = 1140 bits (2949), Expect = 0.0

Identities = 620/766 (80%), Positives = 666/766 (86%), Gaps = 5/766 (0%)

Query: 5 ALLPELWTEILVPICAVIGIAFSLFQWYVVS RVKLTSDLXXXXXXXXXXXXXXXXXDYLIE

64

A+L ++ TE+L+PI A+IGI FS+ QW +V+RVKL

D LIE

Sbjct: 2 AILSDVATEVLIPIAAIIGIGFSIAQWVLVARVKLAPS-----QPGASRSKDGYGDSLIE 56

Query: 65

EEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXLGSVEGFSTD 124

EEEG+ND +VAKCAEIQ AI+EGATSFLFTEY+Y LGSVEGFST

Sbjct: 57 EEEGLNDHNVVAKCAEIQNAIAEGATSFLFTEYQYVGVFMSIFAVVIFLFLGSVEGFSTK
116

Query: 125

NKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLGFLGMKIATYANARTTLEARKGVG 184

PCTY + CKPAL A FST++F+LGA+TSV+SGFLGMKIATYANARTTLEARKGVG

Sbjct: 117

THPCTYSKDKECKPALFNALFSTVSFLLGAITSVSGFLGMKIATYANARTTLEARKGVG 176

Query: 185

KAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMALF 244

KAFI AFRSGAVMGFLLA++GLLVLYI IN+FK+YYGDDWEGLFE+ITGYGLGGSSMALF

Sbjct: 177

KAFITAFRSGAVMGFLLASNGLLVLYIAINLFKMYYGDDWEGLFESITGYGLGGSSMALF 236

Query: 245

GRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYA 304

GRVGGGIYTKAADVGA LVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYA

Sbjct: 237

GRVGGGIYTKAADVGAGLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYA 296

Query: 305 EASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEIEPA
364

E+SCAALVVASISSFGINHDFT MCYPLL+SSMGI+VCLITTLFATDFFEIK VKEIEP+

Sbjct: 297 ESSCAALVVASISSFGINHDFTGMCYPLLSSMGIIVCLITTLFATDFFEIKAVKEIEPS
356

Query: 365 LKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVKNWQLFLCVCVGLWAGLIIGF
424

LK QLIIST +MTVGIA+VSW+ LP FTIFNFG QK V NW LFLCV +GLWAGLIIG+

Sbjct: 357 LKKQLIISTALMTVGIALVSWLALPYKFTIFNFGGEQKEVTNWGLFLCVSIGLWAGLIIGY
416

Query: 425

VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXMY 484

VTEYYTSNAYSPVQDVAD+CRTGAATNVIFGLALGYK MY

Sbjct: 417 VTEYYTSNAYSPVQDVADACRTGAATNVIFGLALGYKSVIIPFAIALGIYVSFTIAAMY
476

Query: 485

GVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIG 544

G+AVAALGMLSTIATGL+IDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIG

Sbjct: 477

GIAVAALGMLSTIATGLSIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIG 536

Query: 545

KGFAIGSAALVSLALFGAFVSRAGIHTVDLTPKVIIGLLVGAMLPYWFSAMTMKSVGSA 604

KGFAIGSAALVSLALFGAFVSRAG+ VDL+PKVIIGL+VGAMLPYWFSAMTMKSVGSA

Sbjct: 537

KGFAIGSAALVSLALFGAFVSRAGVKVVDVLSPKVIIGLIVGAMLPYWFSAMTMKSVGSA 596

Query: 605

ALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFF 664

ALKMVEEVRRQFNTIPGLMEGT KPDYA CVKISTDASIK+MIPPG LVMLTPLIVG F

Sbjct: 597

ALKMVEEVRRQFNTIPGLMEGTGKPDYANCVKISTDASIKQMIPPGALVMLTPLIVGTLF 656

Query: 665

GVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAWSLGPKESEPHKAAV 724

GV+TLSGVLAG+LVSGVQ+AISASNTGGAWDNAKKYIEAG SEHA+SLGPKESE+ HKAAV

Sbjct: 657

GVQTLSGVLAGALVSGVQVAISASNTGGAWDNAKKYIEAGASEHARSLGPKESEPHKAAV 716

Query: 725 IGDITGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

IGDITGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFK F

Sbjct: 717 IGDITGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKLF 762

□ >gi|38045977|gb|AAR08913.1| pyrophosphate-energized vacuolar membrane proton pump
[Thellungiella salsuginea]
Length = 771

Score = 1279 bits (3310), Expect = 0.0

Identities = 695/771 (90%), Positives = 708/771 (91%), Gaps = 1/771 (0%)

Query: 1 MVAPALLPELWTEILVPICAVIGIAFSLFQWYVVSrvKLTSD-LXXXXXXXXXXXXXXXXXX
59

MVA A LPELWTEILVP+CAVIGIAFSLFQW++VSRV++T+D

Sbjct: 1

MVASAFLPELWTEILVPVCAVIGIAFSLFQWFIVSRVRVTADQGASSSSGGSNNGKNGYG 60

Query: 60

DYLIEEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXXLGSVE 119

DYLIEEEEG+N+QSVVAKCAEIQTASEGATSFLFTEYKY LGSVE

Sbjct: 61 DYLIEEEGLNEQSVVAKCAEIQTASEGATSFLFTEYKYVGVFMVFFAAIFVFLGSVE
120

Query: 120

GFSTDNKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEA 179

GFST NKPCTYD T+TCKPALATAAFST+AFVLGAVTSVLSGFLGMKIATYANARTTLEA

Sbjct: 121

GFSTKNKPCTYDDTKTCKPALATAAFSTVAFVLGAVTSVLSGFLGMKIATYANARTTLEA 180

Query: 180

RKGVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGS 239

RKGVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIY BDWEGLFEAITGYGLGGS

Sbjct: 181

RKGVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYXXBDWEGLFEAITGYGLGGS 240

Query: 240

SMALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDL 299

SMALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDL

Sbjct: 241

SMALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDL 300

Query: 300 FGSYAEASCAALVVASISSFGINHDF TAMCYPLLISSMGILVCLITTLFATDFFEIKLVK
359

FGSYAEASCAALVVASISSFGINHDF TAM YPLLISSMGILVCLITTLFATDFFEIK VK

Sbjct: 301 FGSYAEASCAALVVASISSFGINHDF TAML YPLLISSMGILVCLITTLFATDFFEIKAVK
360

Query: 360

EIEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKWQLFLCVCVGLWAG 419

EIEPALKNQLIISTVIMTVGIAIVSWVGLP+SFTIFNFGTQKVVKWQLFLCVCVGLWAG

Sbjct: 361 EIEPALKNQLIISTVIMTVGIAIVSWVGLPSSFTIFNFGTQKVVKWQLFLCVCVGLWAG
420

Query: 420

LIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXX 479

LIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 421 LIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIIPFIAIASIFVSFS
480

Query: 480

XXXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNT 539

MYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNT

Sbjct: 481

FAAMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNT 540

Query: 540

TAAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMK 599

TAAIGKGFAIGSAALVSLALFGAFVSRAG+HTVDVLT PKVIIGLLVGAMLPYWFSAMTMK

Sbjct: 541

TAAIGKGFAIGSAALVSLALFGAFVSRAGVHTVDVLT PKVIIGLLVGAMLPYWFSAMTMK 600

Query: 600

SVGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLI 659

SVGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLI

Sbjct: 601

SVGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLI 660

Query: 660

VGFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAksLGPKGSEP 719
VGFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAksLGPKGSEP

Sbjct: 661

VGFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAksLGPKGSEP 720

Query: 720 HKAaVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

HKAaVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKY

Sbjct: 721 HKAaVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYL 771



>gi|38488590|dbj|BAD02277.1| vacuolar proton pyrophosphatase [Oryza sativa (japonica
cultivar-group)]

Length = 770

Score = 1175 bits (3039), Expect = 0.0

Identities = 638/770 (82%), Positives = 676/770 (87%)

Query: 1

MVAPALLPELWTEILVPICAVIGIAFSLFQWYVVSrvKLTSDLXXXXXXXXXXXXXXXXXXD 60

M A A+LPEL ++++P+ A +GIAF++ QW +VS+VKLT++ D

Sbjct: 1

MAAAAILPELAAQVVIPVAAAVGIAFAVLQWALVSKVKLTAEPRRGEAGGAAGGKSGPSD 60

Query: 61

YLIEEEEGVNDQSVVAKCAEIQTaISEGATSFLFTEYKYXXXXXXXXXXXXXXXXXLSGVEG 120

YLIEEEEG+ND +VV+KCAEIQTaISEGATSFLFTEYKY LSGVEG

Sbjct: 61 YLIEEEEGLNHDHNVVSKCAEIQTaISEGATSFLFTEYKYVGLFMSIFAVLIFLFLGSVEG
120

Query: 121

FSTDNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLsgFLGMKIATYANARTTLEAR 180

FST ++PC Y +TCKPALA A FSTIAFVLGAVTS++SGFLGMKIATYANARTTLEAR

Sbjct: 121

FSTKSQPCHYSKDKTCKPALANAIFSTIAFVLGAVTSVLsgFLGMKIATYANARTTLEAR 180

Query: 181

KGVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS 240

KGVGKAFI AFRSGAVMGFLLAASGLLVLYI IN+F IYYGDDWEGLFEAITGYGLGGSS

Sbjct: 181

KGVGKAFITAFRSGAVMGFLLAASGLLVLYIAINLFGIYYGDDWEGLFEAITGYGLGGSS 240

Query: 241

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF 300

MALFGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF

Sbjct: 241

MALFGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF 300

Query: 301 GSYAEASCAALVVASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKE
360

GSYAE+SCAALVVASISSFGINH+FT M YPLL+SS+GI+ CLITTLFATDFFEIK V E

Sbjct: 301 GSYAESSCAALVVASISSFGINHEFTPMVYPLLVS SVGIACLITTLFATDFFEIKAVSE
360

Query: 361

IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGL 420

IEPALK QLIIST MTVGIA+VSW+GLP +FTIFNFG QK V++WQLFLCV VGLWAGL

Sbjct: 361

IEPALKKQLIISTAFMTVGIALVSWLGLPYTFTIFNFGAQKTQVQSWQLFLCVAVGLWAGL 420

Query: 421

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXX 480

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 421 IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAFSIFLSFSL
480

Query: 481

XXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT 540

MYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT

Sbjct: 481

AAMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT 540

Query: 541

AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKV IIGLLVGAMLPYWFSAMTMKS 600

AAIGKGFAIGSAALVSLALFGAFVSRA I TVDVLT PKV IGL+VGAMLPYWFSAMTMKS

Sbjct: 541

AAIGKGFAIGSAALVSLALFGAFVSRAAISTVDVLT PKV FIGLIVGAMLPYWFSAMTMKS 600

Query: 601

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV 660

VGSAALKMVEEVRRQFNTIPGLMEGT KPDYATCVKISTDASIKEMIPPG LVMLTPLIV

Sbjct: 601

VGSAALKMVEEVRRQFNTIPGLMEGTTKPDYATCVKISTDASIKEMIPPGALVMLTPLIV 660

Query: 661

GGFFGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPH 720

G FGVETLSGVLG+LVSGVQIAISASNTGGAWDNAKKYIEAG S HA++LGPKGS+PH

Sbjct: 661

GILFGVETLSGVLGALVSGVQIAISASNTGGAWDNAKKYIEAGASGHARTLGPKGSDPH 720

Query: 721 KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFK F

Sbjct: 721 KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKLF 770



>gi|2129949|pir||S61422 inorganic diphosphatase (EC 3.6.1.1) (clone TVP5) - common tobacco

Length = 764

Score = 1190 bits (3078), Expect = 0.0

Identities = 642/769 (83%), Positives = 680/769 (88%), Gaps = 5/769 (0%)

Query: 2 VAPALLPELWTEILVPICAVIGIAFSLFQWYVVS RVKLTSDLXXXXXXXXXXXXXXXXXXDY

61

+ ALLP+L T+I++P+CAVIGI FS FQWY+VSRVK++S+

D

Sbjct: 1

MGSALLPDLGTQIVIPVCAVIGIVFSSFQWYLVSRVKVSSEHGATSPSSNKNKNGYGDC 60

Query: 62

LIEEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXLGSVEGF 121

LIEEEEG+ND +VVAKCA+IQ AISEGATSFLFTEY+Y LGSVEGF

Sbjct: 61 LIEEEEGINDHNVVAKCADIQNAISEGATSFLFTEYQYVGIFMIAFAILIFLFLGSVEGF
120

Query: 122

STDNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARK 181

ST ++PCTY+ +CKPALATA FST++F+LGA+TSV+SGFLGMKIATYANARTTLEARK

Sbjct: 121 STSSQPCTYNKEKRCKPALATAIFSTVSFLLGAITSVISGFLGMKIATYANARTTLEARK
180

Query: 182

GVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSM 241

GVGKA +V VMGFLLAA+GLLVLYI IN+FK+YYGDDWEGLFEAITGYGLGGSSM

Sbjct: 181 GVGKACLQ-----VMGFLLAANGLLVLYIAINLFKLYYGDDWEGLFEAITGYGLGGSSM
235

Query: 242

ALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG 301

ALFGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG

Sbjct: 236

ALFGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG 295

Query: 302 SYAEASCAALVVASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEI
361

SYAE+SCAALVVASISSFGI+HDFTAMCYPLLISSMGILVCLITTLFATDFFEIK VKEI

Sbjct: 296 SYAESSCAALVVASISSFGIDHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKAVKEI
355

Query: 362

EPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKWQLFLCVCVGLWAGLI 421

EPALKNQLIIST IMTVGIAIV+W LP+SFTIFNFGTQKVVKWQLFLCV VGLWAGLI

Sbjct: 356 EPALKNQLIISTAIMTVGIAIVTWCLPSSFTIFNFGTQKVWKNWQLFLCVAVGLWAGLI
415

Query: 422

IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXXX 481
IGFVTEYYTSNAYSPVQDVADSC TGAATNVIFGLALGYK

Sbjct: 416 IGFVTEYYTSNAYSPVQDVADSCSTGAATNVIFGLALGYKSVIPIFAIAIAIFVSFTFA
475

Query: 482

XMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA 541
M +AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA

Sbjct: 476
AMGYIAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA 535

Query: 542

AIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMKSV 601
AIGKGFAIGSAALVSLALFGAFVSRAGI TVDVLTP+V IGL+VGAMLPYWFSAMTMKSV

Sbjct: 536
AIGKGFAIGSAALVSLALFGAFVSRAGISTVDVLT PQVFIGLIVGAMLPYWFSAMTMKSV 595

Query: 602

GSAALKMVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVG 661
GSAALKMVEEVRQFNTIPGLMEG AKPDYATCVKISTDASIKEMIPPG LVMLTPLIVG

Sbjct: 596
GSAALKMVEEVRQFNTIPGLMEGLAKPDYATCVKISTDASIKEMIPPGALVMLTPLIVG 655

Query: 662

FFFGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHK 721
FFGVETLSGVLG+LVSGVQIAISASNTGGAWDNAKKYIEAG SEHA++LGPKGSEPHK

Sbjct: 656
IFFGVETLSGVLGALVSGVQIAISASNTGGAWDNAKKYIEAGASEHARTLGPKGSEPHK 715

Query: 722 AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFK F

Sbjct: 716 AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKIF 764

☐ >gi|18274925|sp|Q06572|AVP3_HORVU Pyrophosphate-energized vacuolar membrane proton pump
(Pyrophosphate-energized inorganic pyrophosphatase)
(H⁺-PPase)
gi|6012172|dbj|BAA02717.2| inorganic pyrophosphatase [Hordeum vulgare subsp. vulgare]
Length = 762

Score = 1153 bits (2983), Expect = 0.0

Identities = 624/765 (81%), Positives = 671/765 (87%), Gaps = 5/765 (0%)

Query: 5 ALLPELWTEILVPICAVIGIAFSLFQWYVVSrvKLTSDLXXXXXXXXXXXXXXXXXXDYLIE
64

A+L EL TEIL+P+C VIGI F++ QW++VS+VK+T DYLIE

Sbjct: 2 AILGELGTEILIPVCGVIGIVFAVAQWFIVSKVKVTPGAASAAAGAKNGYG---DYLIE 57

Query: 65

EEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXXXLGSVEGFSTD 124

EEEG+ND +VV KCAEIQTASEGATSFLFT Y+Y LGS+EGFST

Sbjct: 58 EEGLNDHNVVVKCAEIQTASEGATSFLFTMYQYVGMFMVFAAIIIFLFLGSIIEGFSTK
117

Query: 125

NKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVG 184

+PCTY + TCKPAL TA FST +F+LGA+TS++SGFLGMKIATYANARTTLEARKGVG

Sbjct: 118 GQPCTY-

SKGTCKPALYTALFSTASFLGAIITSLVSGFLGMKIATYANARTTLEARKGVG 176

Query: 185

KAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMALF 244

KAFI AFRSGAVMGFLL++SGL+VLYITINVFK+YYGDDWEGLFE+ITGYGLGGSSMALF

Sbjct: 177

KAFITAFRSGAVMGFLLSSSGLVLYITINVFKMYYGDDWEGLFESITGYGLGGSSMALF 236

Query: 245

GRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYA 304

GRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYA

Sbjct: 237

GRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYA 296

Query: 305 EASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEIEPA
364

E+SCAALVVASISSFGINHDFTAMCYPLL+SS+GI+VCL+TTLFATDFFEIK EIEPA

Sbjct: 297 ESSCAALVVASISSFGINHDFTAMCYPLLVS SVGIIVCLLTTLFATDFFEIKAANEIEPA
356

Query: 365 LKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVKNWQLFLCVCVGLWAGLIIGF
424

LK QLIIST +MTVG+A++SW+ LP FTIFNFG QK V NW LF CV VGLWAGLIIGF

Sbjct: 357 LKKQLIISTALMTVGVAVISWLALPAKFTIFNFGAQKEVSNWGLFFCVAVGLWAGLIIGF
416

Query: 425

VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXMY 484

VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK MY

Sbjct: 417 VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAVSIYVSFSIAAMY
476

Query: 485

GVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIG 544

G+A+AALGMLST+ATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIG

Sbjct: 477

GIAMAALGMLSTMATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIG 536

Query: 545

KGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKSVGSA 604

KGFAIGSAALVSLALFGAFVSRAG+ VDVL+PKV IGL+VGAMLPYWFSAMTMKSVGSA

Sbjct: 537

KGFAIGSAALVSLALFGAFVSRAGVKVVDVLS PKVFIGLIVGAMLPYWFSAMTMKSVGSA 596

Query: 605

ALKMVVEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFF 664

ALKMVVEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPG LVMLTPLIVG F

Sbjct: 597

ALKMVVEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGALVMLTPLIVGTLF 656

Query: 665

GVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAHSLGPKGSEPHKAAV 724

GVETLSGVLAG+LVSGVQIAISASNTGGAWDNAKKYIEAG SEHA+SLGPKGS+ HKAAV

Sbjct: 657

GVETLSGVLAGALVSGVQIAISASNTGGAWDNAKKYIEAGNSEHARSLGPKGSDCHKAAV 716

Query: 725 IGDITIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKY 769

IGDITIGDPLKDTSGPSLNILIKLMAVESLVFAPFFAT+GG+LFKY

Sbjct: 717 IGDITIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATYGGLLFKY 761



>gi|7436043|pir|T07801 probable inorganic diphosphatase (EC 3.6.1.1) - mung bean
gi|2653446|dbj|BAA23649.1 proton pyrophosphatase [Vigna radiata]

Length = 766

Score = 1178 bits (3047), Expect = 0.0

Identities = 639/769 (83%), Positives = 682/769 (88%), Gaps = 3/769 (0%)

Query: 2 VAPALLPELWTEILVPICAVIGIAFSLFQWYVSRVKLTSDLXXXXXXXXXXXXXXXXXXDY

61

+ A+LP+L TEIL+P+CAVIGIAF+LFQW +VS+VKL++ DY

Sbjct: 1 MGAAILPDLGTEILIPVCAVIGIAFALFQWLLVSKVKLSA---VRDASPNAAAKNGYNDY 57

Query: 62

LIEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXXXLGSVEGF 121

LIEEEGVND +VV KCAEIQTASEGATSFLFTEYKY LGSVEGF

Sbjct: 58 LIEEEGVNDHNVVVKCAEIQTASEGATSFLFTEYKYVGIFMVAFAILIFLGLSVEGF

117

Query: 122

STDNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARK 181

ST + C+YD T+TCKPALATA FST++F+LG VTS++SGFLGMKIATYANARTTLEARK

Sbjct: 118

STSPQACSYDKTKTCKPALATAIFSTVSFLLGGVTSLSVSGFLGMKIATYANARTTLEARK 177

Query: 182

GVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSM 241

GVGKAFI AFRSGAVMGFLLAA+GLLVLYI IN+FKIYYGDDW GLFEAITGYGLGGSSM

Sbjct: 178

GVGKAFITAFRSGAVMGFLLAANGLLVLYIAINLFKIYYGDDWGGLFEAITGYGLGGSSM 237

Query: 242

ALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG 301

ALFGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG

Sbjct: 238

ALFGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG 297

Query: 302 SYAEASCAALVVASISSFGINHDF TAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEI

361

SYAE+SCAALVVASISSFG+NH+ TAM YPL++SS+GILVCL+TTLFATDFFEIK VKEI

Sbjct: 298 SYAESSCAALVVASISSFGLNHEL TAMLYPLIVSSVGILVCLITTLFATDFFEIKAVKEI

357

Query: 362

EPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGLI 421

EPALK QL+ISTV+MT+G+A+VS+V LPTSFTIFNFG QK VK+WQLFLCV VGLWAGLI

Sbjct: 358

EPALKKQLVISTVLMTIGVAVVSFVALPTSFTIFNFGVQKDVKSWQLFLCVAVGLWAGLI 417

Query: 422

IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXX 481

IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 418 IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIASIFVSFTLA

477

Query: 482

XMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA 541
MYG+AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA

Sbjct: 478

AMYGIAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA 537

Query: 542

AIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMKSV 601

AIGKGFAIGSAALVSLALFGAFVSR I TVDVLTPKV IGL+VGAMLPYWFSAMTMKSV

Sbjct: 538 AIGKGFAIGSAALVSLALFGAFVSRASITTVDVLTPKVFGLIVGAMLPYWFSAMTMKSV
597

Query: 602

GSAALKMVVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVG 661

GSAALKMVVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPG LVMLTPL+VG

Sbjct: 598

GSAALKMVVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGALVMLTPLVVG 657

Query: 662

FFFGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHK 721

FGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAG SEHA+SLGPKGS+ HK

Sbjct: 658

ILFGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGASEHARSLGPKGSDCHK 717

Query: 722 AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGG+LFK F

Sbjct: 718 AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGLLFKIF 766



>gi|15218279|ref|NP_173021.1| pyrophosphate-energized vacuolar membrane proton
pump /

pyrophosphate-energized inorganic pyrophosphatase

(AVP-3) [Arabidopsis thaliana]

gi|399091|sp|P31414|AVP3_ARATH Pyrophosphate-energized vacuolar membrane proton
pump

(Pyrophosphate-energized inorganic pyrophosphatase)

(H⁺-PPase)

[gi|282878|pir|A38230](#) inorganic diphosphatase (EC 3.6.1.1), H⁺-translocating

pyrophosphate-energized - *Arabidopsis thaliana*

[gi|166634|gb|AAA32754.1|](#) vacuolar H⁺-phosphatase

[gi|8927648|gb|AAF82139.1|](#) Identical to Vacuolar proton pyrophosphatase (AVP3) from

Arabidopsis thaliana [gb|AB015138](#) and [gb|M81892](#). ESTs

[gb|AA006922](#), [gb|AA586042](#), [gb|AA651053](#), [gb|AA712863](#),

[gb|AA394384](#), [gb|AA605347](#), [gb|AA006474](#), [gb|AA006772](#),

[gb|AA650817](#), [gb|AA042538](#), [gb|AA006217](#), [gb|AW004149](#),

[gb|H36252](#), [gb|H36659](#), [gb|R30444](#), [gb|W43600](#), [gb|W43886](#),

[gb|W43517](#), [gb|W43127](#), [gb|N96656](#), [gb|T14167](#), [gb|T76140](#),

[gb|T21188](#), [gb|Z17694](#), [gb|Z17695](#) come from this gene

[gi|27311751|gb|AAO00841.1|](#) Unknown protein [*Arabidopsis thaliana*]

Length = 770

Score = 1316 bits (3405), Expect = 0.0

Identities = 718/770 (93%), Positives = 718/770 (93%)

Query: 1

MVAPALLPELWTEILVPICAVIGIAFSLFQWYVVS RVKLTSDLXXXXXXXXXXXXXXXXXXXXD 60

MVAPALLPELWTEILVPICAVIGIAFSLFQWYVVS RVKLTSDL D

Sbjct: 1

MVAPALLPELWTEILVPICAVIGIAFSLFQWYVVS RVKLTSDLGASSSGGANNGKNGYGD 60

Query: 61

YLIEEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXXXLGSVEG 120

YLIEEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKY LGSVEG

Sbjct: 61 YLIEEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYVGVFMIFFAAVIFVFLGSVEG

120

Query: 121

FSTDNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVL SGFLGMKIATYANARTTLEAR 180

FSTDNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVL SGFLGMKIATYANARTTLEAR

Sbjct: 121

FSTDNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVL SGFLGMKIATYANARTTLEAR 180

Query: 181

KGVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS 240

KGVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS

Sbjct: 181

KGVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS 240

Query: 241

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF 300

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF

Sbjct: 241

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF 300

Query: 301 GSYAEASCAALVVASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKE
360

GSYAEASCAALVVASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKE

Sbjct: 301 GSYAEASCAALVVASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKE
360

Query: 361

IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKWQFLCVCVGLWAGL 420

IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKWQFLCVCVGLWAGL

Sbjct: 361 IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKWQFLCVCVGLWAGL
420

Query: 421

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXX 480

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 421 IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAISIFVSFSF
480

Query: 481

XXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT 540

MYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT

Sbjct: 481

AAMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT 540

Query: 541

AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMKS 600

AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMKS

Sbjct: 541

AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMKS 600

Query: 601

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV 660

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV

Sbjct: 601

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV 660

Query: 661

GFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA KSLGPKGSEPH 720

GFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA KSLGPKGSEPH

Sbjct: 661

GFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA KSLGPKGSEPH 720

Query: 721 KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF

Sbjct: 721 KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770



>gi|1076627|pir|S54172 inorganic diphosphatase (EC 3.6.1.1) - common tobacco

gi|790479|emb|CAA58701.1| inorganic pyrophosphatase [Nicotiana tabacum]

Length = 765

Score = 1203 bits (3113), Expect = 0.0

Identities = 650/769 (84%), Positives = 686/769 (89%), Gaps = 4/769 (0%)

Query: 2 VAPALLPELWTEILVPICAVIGIAFSLFQWYVVS RVKLTSDLXXXXXXXXXXXXXXXXXXDY

61

+ ALLP+L EI++P+CAVIGI FSL QWY+VS VKLT + DY

Sbjct: 1 MGAALLPDLGAEIVPVCVIGIVFSLVQWYLVSNVKLTPE----SSSPSNNGKNGYGDY

56

Query: 62

LIEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXX LGSVEGF 121

LIEEEG+N+Q+VV KCAEIQ AISEGATSFLFTEY+Y LGSVEGF

Sbjct: 57 LIEEEGINEQNWWWKCAEIQNAISEGATSFLFTEYQYVGIFMIAFAILIFLFLGSVEGF
116

Query: 122

STDNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARK 181

ST ++PCTY+ +CKPALATA FST++F+LGAVTSV+SGFLGMKIATYANARTTLEARK

Sbjct: 117
STKSQPCTYNKEKLCKPALATAIFSTVSFLLGAVTSVVSGFLGMKIATYANARTTLEARK 176

Query: 182

GVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSM 241

GVGKAFIVAFRSGAVMGFLLAA+GLLVLYI IN+FK+YYGDDWEGLFEAITGYGLGGSSM

Sbjct: 177
GVGKAFIVAFRSGAVMGFLLAANGLLLVLYIAINLFKLYYGDDWEGLFEAITGYGLGGSSM 236

Query: 242

ALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG 301

ALFGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG

Sbjct: 237
ALFGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG 296

Query: 302 SYAEASCAALVVASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEI
361

SYAEASCAALVVASISSFGINH+FTAM YPLLISSMGIL+CLITTLFATDFFEIK VKEI

Sbjct: 297 SYAEASCAALVVASISSFGINHEFTAMLYPLLISSMGILICLITTLFATDFFEIKAVKEI 356

Query: 362

EPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKWQFLFCVGVGLWAGLI 421

EPALKNQLIIST +MTVGIAIV+W LP+SFTIFNFG QKVVKWQFLFCV VGLWAGLI

Sbjct: 357 EPALKNQLIISTALMTVGIAIVTWTCLPSSFTIFNFGAQKVVKWQFLFCVAVGLWAGLI
416

Query: 422

IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXX 481

IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 417 IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIIPFAIAIAIFVSFSFA
476

Query: 482

XMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA 541

MYG+AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA

Sbjct: 477

AMYGIAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA 536

Query: 542

AIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTTPKVIIGLLVGAMLPYWFSAMTMKSV 601

AIGKGFAIGSAALVSLALFGAFVSRA I TVDVLTP+V IGL+VGAMLPYWFSAMTMKSV

Sbjct: 537

AIGKGFAIGSAALVSLALFGAFVSRAAITTVDVLTPQVFIGLIVGAMLPYWFSAMTMKSV 596

Query: 602

GSAALKMVVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVG 661

GSAALKMVVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPG LVMLTPLIVG

Sbjct: 597

GSAALKMVVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGALVMLTPLIVG 656

Query: 662

FFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHK 721

FFGVETLSGVLAG+LVSGVQIAISASNTGGAWDNAKKYIEAG SEHA++LGPKGS+PHK

Sbjct: 657

IFFGVETLSGVLAGALVSGVQIAISASNTGGAWDNAKKYIEAGASEHARTLGPKGSDPHK 716

Query: 722 AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGG+LFK F

Sbjct: 717 AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGLLFKIF 765

☐ >gi|19310433|gb|AAL84953.1| At1g15690/F7H2_3 [Arabidopsis thaliana]
Length = 770

Score = 1314 bits (3400), Expect = 0.0
Identities = 717/770 (93%), Positives = 717/770 (93%)

Query: 1

MVAPALLPELWTEILVPICAVIGIAFSLFQWYVVSrvKLTSDLXXXXXXXXXXXXXXXXXXD 60
MVAPALLPELWTEILVPICAVIGIAFSLFQWYVVSrvKLTSDL D

Sbjct: 1

MVAPALLPELWTEILVPICAVIGIAFSLFQWYVVSrvKLTSDLGASSSGGANNGKNGYGD 60

Query: 61

YLIEEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXXXLGSVEG 120
YLIEEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKY LGSVEG

Sbjct: 61 YLIEEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYVGVFMIFFAAVIFVFLGSVEG
120

Query: 121

FSTDNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLsgFLGMKIATYANARTTLEAR 180
FSTDNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLsgFLGMKIATYANARTTLEAR

Sbjct: 121

FSTDNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLsgFLGMKIATYANARTTLEAR 180

Query: 181

KGVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS 240
KGVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS

Sbjct: 181

KGVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS 240

Query: 241

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF 300
MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF

Sbjct: 241

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF 300

Query: 301 GSYAEASCAALVVASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKE
360

GSYAEASCAALVVASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKE
Sbjct: 301 GSYAEASCAALVVASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKE
360

Query: 361

IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVKNWQLFLCVCVGLWAGL 420
IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVKNWQLFLCVCVGLWAGL
Sbjct: 361 IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVKNWQLFLCVCVGLWAGL
420

Query: 421

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXX 480
IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK
Sbjct: 421 IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIIPFAIAISIFVSFSF
480

Query: 481

XXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT 540
MYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT
Sbjct: 481
AAMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT 540

Query: 541

AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMKS 600
AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMKS
Sbjct: 541
AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMKS 600

Query: 601

VGSAALKMVVEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV 660
VGSAALKMVVEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV
Sbjct: 601
VGSAALKMVVEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV 660

Query: 661

GFFFGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAHSLGPKGSEPH 720
GFFFGVETLSGVLGSLVSGVQIA SASNTGGAWDNAKKYIEAGVSEHAHSLGPKGSEPH

Sbjct: 661

GFFFGVETLSGVLGSLVSGVQIATSASNTGGAWDNAKKYIEAGVSEHAHSLGPKGSEPH 720

Query: 721 KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF

Sbjct: 721 KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

☐ >gi|34894952|ref|NP_908801.1| putative H⁺-pyrophosphatase [Oryza sativa (japonica
cultivar-group)]
gi|15290183|dbj|BAB63873.1| putative H⁺-pyrophosphatase [Oryza sativa (japonica
cultivar-group)]
Length = 773

Score = 994 bits (2569), Expect = 0.0

Identities = 545/768 (70%), Positives = 625/768 (81%), Gaps = 12/768 (1%)

Query: 13 EILVPICAVIGIAFSLFQWYVVSrvKLTS-----DLXXXXXXXXXXXXXXXXXD 60

+ ++P CA +GIAF+++QW +VSRVK++

Sbjct: 6

DAVIPACAAVGIAFAVWQWLLVSRVKVSPYSAAAAAARNGGAGRAVFRPEGEVDDDDGGC 65

Query: 61

YLIEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXLGSVEG 120

EE +G + +A+CAEIQ+AI GA SFLFT+YKY LGSV

Sbjct: 66

GDDEEADGDGGVAAMARCAEIQSIRVGANSFLFTQYKYLAFTAVFAVVIFLFLGSVHR 125

Query: 121

FSTDNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLGFLGMKIATYANARTTLEAR 180

FST+++PC Y + CKPALA A FSTIAF+LGA TSV SGFLGM+IAT ANARTT+EAR

Sbjct: 126

FSTESQPCQYTRGKACKPALANAVFSTIAFLLGAATSVASGFLGMRIATAANARTTVEAR 185

Query: 181

KGVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS 240

+G+G AF AFRSGAVMGFLLA+ GLLVLY+ I VF +YYGDDWEGL+E+ITGYGLGGSS

Sbjct: 186

RGIGPAFAAAFRSGAVMGFLLASLGLLVLYVAIKVFLYYGDDWEGLYESITGYGLGGSS 245

Query: 241

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF 300

MALFGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF

Sbjct: 246

MALFGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF 305

Query: 301 GSYAEASCAALVVASISSFGINHFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKE
360

GSYAE++CAAL V SISSFG +H+F A+ YPLLISS G++VCLITTLFATD + +K V

Sbjct: 306 GSYAESTCAALFVGSISSFGADHNFAAVSYPLLISSAGLIVCLITTLFATDLYRVKTVDG
365

Query: 361

IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGL 420

+ PALK QL+ISTV+MTVG+ +V++ LP FT+F+FG K VKNW LF CV +GLWAGL

Sbjct: 366

VAPALKLQLLISTVLMTVGVLVVTF TALPHEFTMFDFGEVKRVKNWHLFFCVTIGLWAGL 425

Query: 421

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXX 480

IGF TEY+TSNAYSPV+DVADSCRTGAATNVIFGLALGYK

Sbjct: 426 AIGFTTEYFTSNAYSPVRDVADSCRTGAATNVIFGLALGYKSVIVPVFAIAVSIYVSFTL
485

Query: 481

XXMYGVAVALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT 540

+YG+AVAALGMLST+ATGLAIDAYGPISDNAGGIAEMAGMSHRIR+RTDALDAAGNTT

Sbjct: 486

ASIYGIABAALGMLSTVATGLAIDAYGPISDNAGGIAEMAGMSHRIRQRTDALDAAGNTT 545

Query: 541

AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDLTPKVIIGLLVGAMLPYWFSAMTMKS 600

AAIGKGFAIGSAALVSLALFGAFVSRAG+ ++VL+PKV +GL+VGAMLPYWFSAMTMKS

Sbjct: 546

AAIGKGFAIGSAALVSLALFGAFVSRAGMAVINVLSPKVFVGLVVGAMLPYWFSAMTMKS 605

Query: 601

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV 660

VGSAALKMVEEVRRQF IPGLMEG A PDYA+CV+ISTDAS++EM+PPG LV+L PL+

Sbjct: 606

VGSAALKMVEEVRRQFAAIPGLMEGRATPDYASCVRISTDASLREMMPPGALVLLAPLVA 665

Query: 661

GFFFGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPH 720

G FFGV+TL+G+LAG+LVSGVQ+AISASN+GGAWDNAKKYIEAG S+HAK+LGPKGS+ H

Sbjct: 666

GTFFGVQTLAGLLAGALVSGVQVAISASNSGGAWDNAKKYIEAGASDHAKALGPKGSDAH 725

Query: 721 KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFK 768

KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFA HGG++FK

Sbjct: 726 KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFAAHGGGLIFK 773

☐ >gi|33465893|gb|AAQ19328.1| H+-pyrophosphatase [Oryza sativa (japonica cultivar-group)]

Length = 773

Score = 991 bits (2561), Expect = 0.0

Identities = 543/768 (70%), Positives = 624/768 (81%), Gaps = 12/768 (1%)

Query: 13 EILVPICAVIGIAFSLFQWYVVSrvKLTS-----DLXXXXXXXXXXXXXXXXXD 60

+ ++P CA +GIAF+++QW +VSRVK++

Sbjct: 6

DAVIPACAAVGIAFAVWQWLLVSRVKVSPYSAAAAAARNGGAGRAVFRPEGEVDDDDGGC 65

Query: 61

YLIEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXXLGSVEG 120

E +G + +A+CAEIQ+AI GA SFLFT+YKY LGSV

Sbjct: 66

GDDEGADGDGGVAAMARCAEIQSAIRVGANSFLFTQYKYLAFTAVFAVVIFLFLGSVHR 125

Query: 121

FSTDNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLGFLGMKIATYANARTTLEAR 180

FST+++PC Y + CKPALA A FSTIAF+LGA TSV SGFLGM+IAT ANARTT+EAR

Sbjct: 126

FSTESQPCQYTRGKACKPALANAVFSTIAFLLGAATSVASGFLGMRIATAANARTTVEAR 185

Query: 181

KGVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS 240

+G+G AF AFRSGAVMGFLLA+ GLLVLY+ I VF +YYGDDWEGL+E+ITGYGLGGSS

Sbjct: 186

RGIGPAFAAAFRSGAVMGFLLASLGLLVLYVAIKVFGLYYGDDWEGLYESITGYGLGGSS 245

Query: 241

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF 300

MALFGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF

Sbjct: 246

MALFGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLF 305

Query: 301 GSYAEASCAALVVASISSFGINHFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKE
360

GSYAE++CAAL V SISSFG +H+F A+ YPLLISS G++VCLITTLFATD + +K V

Sbjct: 306 GSYAESTCAALFVGSISSFGADHNFAAVSYPLLISSAGLIVCLITTLFATDLRYRVKTVDG
365

Query: 361

IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGL 420

+ PALK QL+ISTV+MTVG+ +V++ LP FT+F+FG K VKNW LF CV +GLWAGL

Sbjct: 366

VAPALKLQLLISTVLMTVGVLVVTF TALPHEFTMFDFGEVKRVKNWHLFFCVTIGLWAGL 425

Query: 421

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXX 480

IGF TEY+TSNAYSPV+DVADSCRTGAATNVIFGLALGYK

Sbjct: 426 AIGFTTEYFTSNAYSPVRDVADSCRTGAATNVIFGLALGYKSVIVPVFAIAVSIYVSFTL
485

Query: 481

XXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT 540

+YG+AVAALGMLST+ATGLAIDAYGPISDNAGGIAEMAGMSHRIR+RTDALDAAGNTT

Sbjct: 486

ASIYGIABAALGMLSTVATGLAIDAYGPISDNAGGIAEMAGMSHRIRQRTDALDAAGNTT 545

Query: 541

AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMKS 600

AAIGKGFAIGSAALVSLALFGAFVSRAG+ ++VL+PKV +GL+VGAMLPYWFSAMTMKS

Sbjct: 546

AAIGKGFAIGSAALVSLALFGAFVSRAGMAVINVLSPKVFVGLVVGAMLPYWFSAMTMKS 605

Query: 601

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV 660

VGSAALKMVEEVRR+F IPGLMEG A PDYA+CV+ISTDAS++EM+PPG LV+L PL+

Sbjct: 606

VGSAALKMVEEVRREFAAIPGLMEGRATPDYASCVRISTDASLREMMPPGALVLLAPLVA 665

Query: 661

GFFFGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPH 720

G FFGV+TL+G+LAG+LVSGVQ+AISASN+GGAWDNAKKYIEAG S+HAK+LGPKGS+ H

Sbjct: 666

GTFFGVQTLAGLLAGALVSGVQVAISASNSGGAWDNAKKYIEAGASDHAKALGPKGSDAH 725

Query: 721 KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFK 768

KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFA HGG++FK

Sbjct: 726 KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFAAHGGILFK 773

☐ >gi|4126976|dbj|BAA36841.1| vacuolar H⁺-pyrophosphatase [Chara corallina]
Length = 793

Score = 941 bits (2433), Expect = 0.0

Identities = 510/755 (67%), Positives = 588/755 (77%), Gaps = 14/755 (1%)

Query: 14

ILVPICAVIGIAFSLFQWYVVSRLKLTSDLXXXXXXXXXXXXXXXXXDYLIEEEEGVNDQS 73

I +P VIGI F++ QW VV ++ + +Y + +EG+ D S

Sbjct: 41 IFIPAAACVIGILFAVLQWSVVGKISVRPS-----GGGMNYPLMGDEGLEDDSS 87

Query: 74

VWAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXXLGSVEGFSTDNKPCTYDTT 133

VV +CAEIQ AISEGA SFL TEYKY LG+ E F TD KPC +D T

Sbjct: 88

VVTRCAEIQEASEGAVSFLMTEYKYLSYFMVGFFIVIFAFLGATEDFGTDRKPCWDAT 147

Query: 134

RTCKPALATAAFSTIAFVLGAVTSVLGFLGMKIATYANARTTLEARKGVGKAFIVAFRS 193

+ C + A S +AF LGA+TS L GFLGMKIAT+ANART GVG AF AFRS

Sbjct: 148

KLCGSGVMNALLSAVAFALGAIITSTLCGFLGMKIATFANARTRSRRGGGVGPAFKAAFRS 207

Query: 194

GAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMALFGRVGGGIYT 253

GAVMGFLL + GL+VLY TI +F+ YYGDDW GL+E+I GYGLGGSS+ALFGRVGGGIYT

Sbjct: 208

GAVMGFLLTSLGLIVLYFTILIFQRYYGDDWIGLYESIAGYGLGGSSVALFGRVGGGIYT.267

Query: 254

KAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAEASCAALVW 313

KAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMG+DLFGS AE++CAALVW

Sbjct: 268

KAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGADLFGSLAESTCAALVW 327

Query: 314 ASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFE-IKLVKEIEPALKNQLIIS 372
+S+S FG ++ AM +PLLI+ GILVCLITTL ATD + +K IEPALK QL+IS
Sbjct: 328 SSLSDFGKEMNYVAMSFPLITGAGILVCLITTLVATDLTSGVSNIKGIEPALKQQLVIS
387

Query: 373
TVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGLIIGFVTEYYTSN 432
TV+MT IA+++W LP +F I N KVK W +F CV GLWAGL+IG+ TEY+TS+
Sbjct: 388
TVLMTPVIALLOWGCLPDTFEIINGAETKVVKWYMFFCVACGLWAGLLIGYTTEYFTSH 447

Query: 433
AYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXXMYGVAVAALG 492
++PV+DVADSCRTGAATNVIFGLALGYK MYG+A AALG
Sbjct: 448 QFTPVRDVADSCRTGAATNVIFGLALGYKSVIPIAIAFTVFSHTLAAMYGIACAALG
507

Query: 493
MLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIGKGFAIGSA 552
MLST++T LAIDAYGPISDNAGGIAEMA M IRE+TDALDAAGNTTAAIGKGFAIGSA
Sbjct: 508
MLSTLSTCLAYGPISDNAGGIAEMAEMGPAIREKTDALDAAGNTTAAIGKGFAIGSA 567

Query: 553
ALVSLALFGAFVSRAGIHTVDLTPKVIIGLLVGAMLPYWFSAMTMKSVGSAALKMVEEV 612
ALVSLALFGA+++RAGI +VDV+ PK +GL+VGAMLPYWFSAMTMKSVG AAL MVEEV
Sbjct: 568
ALVSLALFGAYINRAGITSVDVILPKEFVGLIVGAMLPYWFSAMTMKSVGKAALAMVEEV 627

Query: 613
RRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFFGVETLSGV 672
RRQFNTI GLM+GT KPDY CV+ISTDAS++EMIPPGCLVMLTPL+VG G ETL+G+
Sbjct: 628
RRQFNTIAGLMQGTVPDYKRCVEISTDASLREMIPPGCLVMLTPLVVGGLLGKETLAGI 687

Query: 673

LAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHKAAVIGDTIGDP 732

LAG+LVSGVQIAISASNTGGAWDNAKKYIEAG ++HA++LGPKGS+ HKAAVIGDT+GDP

Sbjct: 688

LAGALVSGVQIAISASNTGGAWDNAKKYIEAGGNDHARTLGPKGSDCHKAAVIGDTVGDGP 747

Query: 733 LKDTSGPSLNILIKLMAVESLVFAPFFATHGGILF 767

LKDTSGPSLNILIKLMAVESLVFAPFF T+GG+LF

Sbjct: 748 LKDTSGPSLNILIKLMAVESLVFAPFFKTYGGVLF 782



>gi|45267862|gb|AAS55761.1| putative inorganic diphosphatase (EC 3.6.1.1) [Oryza sativa
(japonica cultivar-group)]

Length = 770

Score = 937 bits (2422), Expect = 0.0

Identities = 531/769 (69%), Positives = 615/769 (79%), Gaps = 3/769 (0%)

Query: 5 ALLPELWTEILVPICAVIGIAFSLFQWYVVS RVKLTSDLXXXXXXXXXXXXXXXXXXDY LIE

64

AL+ + E+L+P+ AVIGI F++ QWY+VSRV +

Sbjct: 2

ALIGTVAAEVLIPLA AVIGILFAVLQWYMVSRVAVPPHDG VGGAGKVERESDGGDGDGDG 61

Query: 65 EE EGVND---

QSVVAKCAEIQT AISEGATSFLFTEYKYXXXXXXXXXXXXXXXXX LGSVEGF 121

++ + + V A+CAEIQ AIS GATSFL TEYKY LGSV F

Sbjct: 62

VDDEEDGVDYRGVEARCAEIQH AISVGATSFLMTEYKYLGA FMAAFAAVIFVSLGSVGRF 121

Query: 122

STDNKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVL SGLGMKIATYANARTTLEARK 181

ST +PC YD R C+PALA AAF+ AF+LGA TSV+SG+LGM++AT+ANART LEAR+

Sbjct: 122

STSTEPCPYDAARRCRPALANAAFTAAAFLLGATT SVVSGYLGMRVATFANARTALEARR 181

Query: 182

GVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSM 241

G+G+AF VAFRSGA MGFLLA+S LLVL+ +N F +YYGDDW GL+EAITGYGLGGSSM

Sbjct: 182

GIGRAFAVAFRSGAAMGFLLASSALLVLFAAVNAFGLYYGDDWGGLYEAITGYGLGGSSM 241

Query: 242

ALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG 301

ALFGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG

Sbjct: 242

ALFGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFG 301

Query: 302 SYAEASCAALVASISSFGINHDF TAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEI

361

SYAE+SCAAL VASISSFG +HDF AM YPLL+S+ GI+ C TTL ATD E+ E+

Sbjct: 302

SYAESSCAALFVASISSFGADHDF AAMMYPLL VSAAGIVACAATTLVATDAGELGADEV 361

Query: 362

EPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVKNWQLFLCVCVGLWAGLI 421

PALK Q++ISTV+MT +A V+++ LP SFT+F+FG +K+VKNW LF+CV GLWAGL+

Sbjct: 362

APALKRQILISTVLMTAAVAAVTFLSLPRSFTLFDFGERKLVKNWHLFICVSAGLWAGLV 421

Query: 422

IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXXX 481

IG+VTEY+TSNAY PVQ VA SCRTGAATNVIFGLA+GYK

Sbjct: 422 IGYVTEYFTSNAYGPVQTVAQSCRTGAATNVIFGLAVGYKSVIVPIFAIAGAIYASFRLA

481

Query: 482

XMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA 541

MYG+A+AALGMLSTIATGL IDAYGPISDNAGGIAEMAGM R+RERTDALDAAGNTTA

Sbjct: 482

AMYGIALAALGMLSTIATGLTIDAYGPISDNAGGIAEMAGMPRRVRERTDALDAAGNTTA 541

Query: 542

AIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIIGLLVGAMLPYWFSAMTMKSV 601

AIGKGFAIGSAALVSLALFGA+VSRAGI TV+V++P+V +GLL GAMLPYWFSAMTM+SV

Sbjct: 542

AIGKGFAIGSAALVSLALFGAYVSRAGIRTVNVVSPRVFVGLLAGAMLPYWFSAMTMRSV 601

Query: 602

GSAALKMVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVG 661

GSAAL+MVEEVRQF+ IPGL EG A PDYATCV+ISTDAS++EM+ PG LVM +PL+ G

Sbjct: 602

GSAALRMVEEVRQFDEIPGLAEGLAAPDYATCVRISTDASLREMVAPGALVMASPLVAG 661

Query: 662

FFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA KSLGPKGSEPHK 721

FGVE L+G+LAG+LVSGVQ+AISASN+GGAWDNAKKYIEAG +E A+SLGPKGSE HK

Sbjct: 662

TLFGVEALAGLLAGALVSGVQVAISASNSGGAWDNAKKYIEAGATEEARS LGPKGSEAHK 721

Query: 722 AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

AAVIGDTIGDPLKDTSGPSLNIL+KLMAVE+LVFAPFFA HGGI+F +

Sbjct: 722 AAVIGDTIGDPLKDTSGPSLNILVKLMAVEALVFAPFFAAHGGIVFNHL 770



>gi|2118183|pir||S61425 inorganic diphosphatase (EC 3.6.1.1), H⁺-translocating (clone TVP17), vacuolar membrane - common tobacco (fragment)

gi|790475|emb|CAA58699.1| inorganic pyrophosphatase [Nicotiana tabacum]

Length = 541

Score = 881 bits (2277), Expect = 0.0

Identities = 479/541 (88%), Positives = 500/541 (92%)

Query: 230

AITGYGLGGSSMALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNV 289

AITGYGLGGSSMALFGRV GGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNV

Sbjct: 1

AITGYGLGGSSMALFGRVAGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNV 60

Query: 290

GDIAGMGSDLFGSYAEASCAALVVASISSFGINHDFAMCYPLLISSMGILVCLITTLFA 349

GDIAGMGSDLFGSYAE+SCAALVVASISSFG+NH+FTAM YPLL+SS+GILVCL+TTLFA

Sbjct: 61

GDIAGMGSDLFGSYAESSCAALVVASISSFGVNHEFTAMLYPLLVS SVGILVCLLTTLFA 120

Query: 350 TDFFEIKLVKEIEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVKNWQLF

409

TDFFE+K VKEIEPALK QL+IST +MT GIA+V+W+ LP++FTIFNFG QK VK+WQLF

Sbjct: 121 TDFFEVKAVKEIEPALKQQLVISTALMTDGIAVVTWIALPSTFTIFNFGAQKEVKS WQLF

180

Query: 410

LCVCVGLWAGLIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXX 469

LCV VGLWAGLIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 181 LCVGVGLWAGLIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKS VIPIFA

240

Query: 470

XXXXXXXXXXXXMYGVAVALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRER 529

MYG+AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRER

Sbjct: 241 IAVSIFVSFSFAAMYGIAVALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRER

300

Query: 530

TDALDAAGNTTAAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAML 589

TDALDAAGNTTAAIGKGFAIGSAALVSLALFGAFVSRA I TVDVLTPKV IGLLVGAML

Sbjct: 301 TDALDAAGNTTAAIGKGFAIGSAALVSLALFGAFVSRAAISTVDVLT PKVFIGLLVGAML

360

Query: 590

PYWFSAMTMKSVGSAALKMVVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPP 649

PYWFSAMTMKSVGSAALKMVVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMI P

Sbjct: 361

PYWFSAMTMKSVGSAALKMVVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIAP 420

Query: 650

GCLVMLTPLIVGFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA 709

G LVMLTPLIVG FGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA

Sbjct: 421

GALVMLTPLIVGILFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA 480

Query: 710

KSLGPKGSEPHKAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKY 769

++LGPKGS HKAAVIGDT+GDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGG+LFK

Sbjct: 481

RTLGPKGSTAHKAAVIGDTVGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGLLFKL 540

Query: 770 F 770

F

Sbjct: 541 F 541

☐ >gi|14970742|emb|CAC44451.1| proton-translocating inorganic pyrophosphatase

[Chlamydomonas

reinhardtii]

Length = 762

Score = 833 bits (2153), Expect = 0.0

Identities = 481/776 (61%), Positives = 574/776 (73%), Gaps = 33/776 (4%)

Query: 8 PELWTEILVPICAVIGIAFSLFQWYVVS RVKLTSDLXXXXXXXXXXXXXXXXXXDYLIEEEE

67

P+ +P AV+ I F++F W V+ +++T +YL+EEE+

Sbjct: 4 PDALIAAFIPASAVVAILFAVFLWKRVA AIQMTG-----GRVLSSQNGREYLLLEEEQ 55

Query: 68

GVNDQSVVAKCAEIQTASEGATSFLFTEYKXXXXXXXXXXXXXXXXXXLGSVEGFSTDNKP 127

++ +VAK A+IQ +ISEGA+SFL TEY Y L V

Sbjct: 56 RGEEEEIVAKAADIQKSISEGASSFLATEYYYLGIFMVIMSVVICSLLSIV----- 106

Query: 128

CTYDTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVGKAF 187

T + RT L FSTIAF LG TS+LSG+LGM+IAT+ANART +EARKG+ AF

Sbjct: 107 -

TPEEGRTSADELNRNGVFSTIAFALGGATSILSGYLGMMQIATFANARTAVEARKGIAPAF 165

Query: 188

IVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMALFGRV 247

+ AFRSGAVMGFLL+ GLL L++ I +F ++GDDW+GLFEAI GYGLGGSS+ALFGRV

Sbjct: 166 MCAFRSGAVMGFLLSGFGLLNLF LAITIFSKFFGDDWKGLFEAI-

GYGLGGSSIALFGRV 224

Query: 248

GGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAEAS 307

GGGIYTKAADVGADLVGK+E++IPEDDPRNPAVIADNVGDNVGDIAGMG+DLFGS+AE++

Sbjct: 225

GGGIYTKAADVGADLVGKVEKDIPEDDPRNPAVIADNVGDNVGDIAGMGADLFGSFAEST 284

Query: 308 CAALVVASISSFGINHDF TAMCYPLLISMGILVCLITTLFATDFFEIKLVKEIEPALKN
367

CAALV++++SS G HD+ M +PLLIS+ GI VCLITT ATD K++ EIE LK

Sbjct: 285 CAALVISAVSSLGKEHDYAGMMFPLLISATGIFVCLITTLATDLKPAKVIAEIEHTLKM
344

Query: 368 QLIISTVIMT-VGIAIVSWVGLPTSFTIFNFGT-----QKVVKNWQLFLCVCVGLWAG
419

QLIIST++MT V ++ W LP FT+ + +KVVK+W +F+C+ GLW G

Sbjct: 345 QLIISTLLMTPVALGVALW-

SLPPEFTLSVPSSSPDKPFDEKVVKSWYMFVCISTGLWGG 403

Query: 420

LIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXXX 479

L++G TEY+TSN Y PVQDVAD+CRTGAAT++IFGLALGYK

Sbjct: 404 LLVGLQTEYFTSNRYKPVQDVADACRTGAATDIIFGLALGYKSCIPTIVIGVAIYVGTS
463

Query: 480

XXXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNT 539
M+G+A ALGMLST+ATGLAIDAYGPISDNAGGIAEMAGM IRERTDALDAAGNT

Sbjct: 464

LAGMFGIACCALGMLSTLATGLAIDAYGPISDNAGGIAEMAGMGEDIRERTDALDAAGNT 523

Query: 540 TAAIGKGFAIGSAALVSLALFGAFVSRAGIHTV--DVLTPKVIIGLLVGAMLPYWFSAMT
597

TAAIGKGFAIGSAALVSLALFGA+V+RAI + +L P+V GLL+GAMLPYWFSAMT

Sbjct: 524

TAAIGKGFAIGSAALVSLALFGAYVTRAKIDMIHSSILDPRVFAGLLLGAAMLPYWFSAMT 583

Query: 598

MKSVGSAALKMVVEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTP 657
MKSVG AAL MV EVRRQFNTI GLMEGTA+PDY CV IST A+I EMI PG LV+ TP

Sbjct: 584

MKSVGKAALAMVHEVRRQFNTIAGLMEGTARPDKRCVAISTQAAISEMIAPGALVIFTP 643

Query: 658

LIVGFFFGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGS 717
++VG FG + L+GVLGSLVSGVQ+A+S SNTGGAWDNAKKYIEAG +EHA+ LG KGS

Sbjct: 644

VVVGALFGTQCLAGVLGSLVSGVQLAVSMSNTGGAWDNAKKYIEAGATEHARELGKGKS 703

Query: 718 EPHKAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFF--ATHG-GILFKYF 770
+ HKAAVIGDT+GDPLKDT+GPSLNILIKLMAVESLVFAPFF HG G++F +F

Sbjct: 704 DCHKAAVIGDTVGDPLKDTNGPSLNILIKLMAVESLVFAPFFYNCAHGQGLIFSFF 759



>gi|1049255|gb|AAA80347.1| H⁺-pyrophosphatase

Length = 509

Score = 815 bits (2106), Expect = 0.0
Identities = 443/507 (87%), Positives = 467/507 (92%)

Query: 225

EGLFEAITGYGLGGSSMALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADN 284
EGLFEAITGYGLGGSSMALFGR+GGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADN

Sbjct: 1

EGLFEAITGYGLGGSSMALFGRLLGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADN 60

Query: 285

VGDNVGDIAGMGSDLFGSYAEASCAALVVASISSFGINHDFAMCYPLLISSMGILVCLI 344
VGDNVGDIAGMGSDLFGSYAE+SCAALVVASISSFGINH+FT M YPLL+SS+GI+ CLI

Sbjct: 61 VGDNVGDIAGMGSDLFGSYAESSCAALVVASISSFGINHEFTPMVYPLLLSSVGIIACLI
120

Query: 345 TTLFATDFFEIKLVKEIEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVK
404

TTLFATDFFEIK V EIEPALK QLIIST++MT+GIA++SW+GLP +FTIFNFG QK V+

Sbjct: 121 TTLFATDFFEIKAVDEIEPALKKQLIISTIVMTIGIALISWLGLPYTFTIFNFGVQKTVQ 180

Query: 405

NWQLFLCVCVGLWAGLIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXX 464
+WQLFLCV VGLWAGL+IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 181

SWQLFLCVAVGLWAGLVIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVI 240

Query: 465

XXXXXXXXXXXXXXXXXXXXMYGVAVALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSH 524
MY VAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSH

Sbjct: 241 IPIFAIAFSIFLSFLAAMYXVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSH
300

Query: 525 RIRERTDALDAAGNTTAAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLL
584

RIRERTDALDAAGNTTAAIGKGFAIGSAALVSL LFGAFVSRA I TVDVLTP+V IGL+

Sbjct: 301 RIRERTDALDAAGNTTAAIGKGFAIGSAALVSLRLFGAFVSRAAISTVDVLTPEVFIGLI
360

Query: 585

VGAMLPYWFSAMTMKSVGSAALKMVVEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIK 644

VGAMLPYWFSAMTMKS+GSAALKMVVEVRRQFNTIPGLMEGT KPDYATCVKISTDASIK

Sbjct: 361

VGAMLPYWFSAMTMKSMGSAALKMVVEVRRQFNTIPGLMEGTTKPDYATCVKISTDASIK 420

Query: 645

EMIPPGCLVMLTPLIVGFFFGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAG 704

EMIPPG LVMLTPLIVG FGVETLSGVLG+LVSGVQIAISASNTGGAWDNAKKYIEAG

Sbjct: 421

EMIPPGALVMLTPLIVGILFGVETLSGVLGALVSGVQIAISASNTGGAWDNAKKYIEAG 480

Query: 705 VSEHAksLGPKGSEPHKAAVIGDTIGD 731

VSEHA++LGPKGS+PHKAAVIGDTIGD

Sbjct: 481 VSEHARTLGPKGSDPHKAAVIGDTIGD 507



>gi|21654895|gb|AAK95376.1| vacuolar-type proton translocating pyrophosphatase 1

[Trypanosoma

brucei]

Length = 826

Score = 692 bits (1786), Expect = 0.0

Identities = 405/779 (51%), Positives = 515/779 (66%), Gaps = 56/779 (7%)

Query: 15

LVPICAVIGIAFSLFQWYVSRVKLTSDLXXXXXXXXXXXXXXXXXXDYLIEEEGVNDQSV 74

++ + + G +F+++ WYV S +K+T Y+I +

Sbjct: 79 IIFLASAFGFSFAMYWWYVASDIKITPGKGNIMRNAHLTDEVMRNVYVISKR----- 130

Query: 75 VAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXXLG----SVEGFSTDNKPCTY

130

+S+GA +FLF EY+Y LG S +G D +P

Sbjct: 131 -----VSDGANAFLEAEYRYMGIFMLGFGALLYFLLGVAMSSPQGEGKDGRRPPV-
179

Query: 131 DTTRTCKPALATAAFSTIAFVLGAVTSVLGFLGMKIATYANARTTLEARKGVGK----
185

+ AAFS AFV+GA TSVL+G++GM+IA Y N+RT + A G G

Sbjct: 180 ----

AVEAPWVNAAFSLYAFVIGAFSTVLGAWIGMRIA VYTNSRTAVMATVGGGSDNDV 235

Query: 186 -----AFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWE---GLFEA 230

AF AFR G MGF L + GL L+ T+ + + Y+GD E LFE

Sbjct: 236

LANGSQSRGYALAFQTAFRGGITMGFALTSIGLFALFCTVKLMQTYFGDSAERLPELFEC 295

Query: 231

ITGYGLGGSSMALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVG 290

+ +GLGGSS+A FGRVGGGIYTKAADVGADLVGK+E+NIPEDD RNP VIAD +GDNVG

Sbjct: 296

VAAFGLGGSSVACFGRVGGGIYTKAADVGADLVGKVEKNIPEDDARNPGVIADCIGDNVG 355

Query: 291 DIAGMGSDLFGSYAEASCAALVVASISSFGINHDTAMCYPLLISSMGILVCLITTLFAT
350

DIAGMGSDLFGS+ EA+CAALV+A+ SS ++ DFT M YPLLI++ GI VC+ T L A

Sbjct: 356 DIAGMGSDLFGSFGEATCAALVIAA-SSAELSADFTCMYPLLITAGGIFVCIGTALLAA
414

Query: 351 DFFEIKLVKEIEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVKNWQLFL
410

+K ++IEP LK+QL++ST+ TV + ++ LP +FT+ T K W+ +

Sbjct: 415 TNSGVKWAEDIEPTLKHQLLVSTIGATVVLVFITAYSLPDAFTVGAVETTK----WRAMV
470

Query: 411

CVCVGLWAGLIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXX 470

CV GLW+GL+IG+ TEY+TSN+Y PVQ++A+SC TGAATN+I+GL+LGY

Sbjct: 471 CVLCGLWSGLLIGYSTYFTSNSYRPVQEIAESCETGAATNIIYGLSLGYISVLPPILAM
530

Query: 471

XXXXXXXXXXXXMYGVAVALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERT 530

+YG A+AALG+LST++ L IDAYGPISDNAGGIAEMA M H IRE T

Sbjct: 531 AFTIYLSHHCAGLYGYALAALGILSTMSIALTIDAYGPISDNAGGIAEMA HMGHEIREIT
590

Query: 531

DALDAAGNTTAAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLP 590

DALDAAGNTTAAIGKGFAIGSAA V+LAL+GA+VSR GI TV++L +V+ GLL+GAMLP

Sbjct: 591
DALDAAGNTTAAIGKGFAIGSAAFVALALYGAYVSRVGISTVNLLDARVMAGLLL GAMLP 650

Query: 591

YWFSAMTMKSVGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPG 650

YWFS+TMKSVG AA+ MV E+RRQF P + GT +PDY +CV I+T A++++M+ P

Sbjct: 651 YWFSALTMKSVGVAAMD MVNEIRRFQD-
PAVAAGTKEPDYESCVNIATGAALQQMVAPA 709

Query: 651

CLVMLTPLIVGFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAK 710

CLVML P++ G FG TL+G+L G+LVSGVQ+AISASNTGGAWDNAKKYIE G K

Sbjct: 710 CLVMLAPIVTGILFGRYTLAGLLPGALVSGVQVAISASNTGGAWDNAKKYIEKG-
GLRDK 768

Query: 711 SLGPKGSEPHKAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATH-GGILFK
768

S G KGS H AAVIGDT+GDPLKDTSGP+LNIL+KLMA+ S+VFAP + GG+L K

Sbjct: 769 SKG-KGSPQHAAVIGDTVGDPLKDTSGPALNILVKLMAIISVVFAPVQSKLGGLLVK
826

☐ >gi|8886133|gb|AAF80381.1| vacuolar-type proton translocating pyrophosphatase 1;

PPase1

[Trypanosoma cruzi]

Length = 816

Score = 681 bits (1757), Expect = 0.0

Identities = 399/781 (51%), Positives = 520/781 (66%), Gaps = 48/781 (6%)

Query: 4 PALLPELWTEILVPICAVIGIAFSLFQWYVVS RVKLTSDLXXXXXXXXXXXXXXXXXXDYLI
63

P L+ T +++ A +G +F+++ WYVVS +++T YL

Sbjct: 67 PPLMSADVTTVIIVTSAALGFSFAMYWWYVSEIRITP-----GKDQGM RNAYLT 116

Query: 64

EEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXXXLGSVEGFST 123

+E V+ I +SEGA +FL+ EY+Y LG +S+

Sbjct: 117 DE-----VMRNVYVISRRVSEGANAFLYAEYRYMGLFMIAFGTLIFFLLGV--AYSS 166

Query: 124

DNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKG- 182

+ +R A AA S +AF +G++TSV +G++GM+IA Y NART + A +G

Sbjct: 167 PQ-----

EGSRPVASPWANAALSLLAFFVGSLTSVFAGWIGMRIAVYTNARTAVMATEGS 221

Query: 183 -----VGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGL---FEAI 231

KAF AFR G MGF L ++GL L++ + V Y+ D E + +E +

Sbjct: 222

EEGDQSLGFAKAFQTAFRGGITMGFALTSAGLFSLFVPVKVIGAYFDDAPENVLNVYECV 281

Query: 232 TGYGLG-

GSSMALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNP AVIADNVGDNVG 290

+GL G+++A F RVGGGIYTKAADVGADLVGK+ERNIPEDD RNP VIAD +GDNVG

Sbjct: 282

AAFGLRVGTAVACFARVGGGIYTKAADVGADLVGKVERNIPEDDARNPGVIADCIGDNVG 341

Query: 291 DIAGMGSDLFGSYAEASCAALVVASISSFGINHDTAMCYPLLISMGILVCLITTLFAT
350

DIAGMGSDLFGS+ + SCA LV+A+ S ++ +FT M YPLLI+++GILVC+ + L

Sbjct: 342 DIAGMGSDLFGSFGQTSCAELVIAA-GSAELSSEFTYMMYPLLITAVGILVCIGSALIVA
400

Query: 351 DFFEIKLVKEIEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFL
410

+ ++ +++EP LK QL+ STV TV + ++ GLP +FT+ T K W+ +

Sbjct: 401 NNSGVQRAEDVEPTLKRQLLFSTVAATVALVFLTDFGLPDTFTVGTATTATK----WRALV
456

Query: 411 CVCVGLWAGLIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGY-
KXXXXXXXXX 469

CV GLW+GLIIG+ TEYYTSNAY PVQ++A++C TGAATN+I+GL+LGY

Sbjct: 457
CVMCGLWSGLIIGYTTEYYTSNAYHPVQEIAEACETGAATNIIYGLSLGYFSVVPILAM 516

Query: 470
XXXXXXXXXXXXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRER 529

+YG A+AALG+LST++ L IDAYGPISDNAGGIAEMA M H IRE

Sbjct: 517 AVTILSASYRMADLYGFALAALGILSTMSIALTIDAYGPISDNAGGIAEMA HMGHEIREI
576

Query: 530
TDALDAAGNTTAAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAML 589

TDALDAAGNTTAAIGKGFAI SAA V+LAL+ A+VSR GI T+++L +V+ GLLVGAML

Sbjct: 577 TDALDAAGNTTAAIGKGFAIASAAFVALALYAAVVS RVGIPTINILDARVMGLLVGAML
636

Query: 590
PYWFSAMTMKSVGSAALKMV EEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPP 649

PY FSA TMKSVG AA+ MV E+RRQF P + EGT +PDY +CV I+T A++++M+ P

Sbjct: 637 PYCFSAFTMKSVGLAAMD MVNEIRRQFQN-
PAIAEGTEEPDYESCVAIATQAALQQM VAP 695

Query: 650
GCLVMLTPLIVGFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA 709

CLVMLTP++VG FG TL+G+L G++VSGVQ+AISASNTGGAWDNAKKYIE G

Sbjct: 696 ACLVMLTPIVGVLFGRYTLAGLLPGAIVSGVQVAISASNTGGAWDNAKKYIEKG-
GLRD 754

Query: 710 KSLGPKGSEPHKAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATH-GGILFK
768

K+ G KGS H AAVIGDT+GDPLKDTSGP+LNILIKLMA+ S+VFAP F + GGI+ +

Sbjct: 755 KNKG-KGSPQHAAVIGDTVGDPLKDTSGPALNILIKLMAIISVVFAPVFESQLGGIIMR
813

Query: 769 Y 769

Y

Sbjct: 814 Y 814

☐ [gi|24214171|ref|NP_711652.1](#) Pyrophosphate-energized vacuolar membrane proton
pump [*Leptospira*

interrogans serovar Lai str. 56601]

[gi|45658133|ref|YP_002219.1](#) H⁺-translocating pyrophosphatase [*Leptospira* interrogans
serovar

Copenhageni str. Fiocruz L1-130]

[gi|33301182|sp|Q8F641|HPPA_LEPIN](#) Pyrophosphate-energized proton pump (Pyrophosphate-
energized

inorganic pyrophosphatase) (H⁺-PPase) (Membrane-bound
proton-translocating pyrophosphatase)

[gi|24195070|gb|AAN48670.1](#) Pyrophosphate-energized vacuolar membrane proton pump
[*Leptospira*

interrogans serovar lai str. 56601]

[gi|45601375|gb|AAS70856.1](#) H⁺-translocating pyrophosphatase [*Leptospira* interrogans
serovar

Copenhageni str. Fiocruz L1-130]

Length = 704

Score = 646 bits (1667), Expect = 0.0

Identities = 381/697 (54%), Positives = 483/697 (69%), Gaps = 38/697 (5%)

Query: 77 KCAEIQTASEGATSFLFTEYKXXXXXXXXXXXXXXXXXXLGS--
VEGFSTDNKPCTYDTTR 134

K EI +AISEGA +FL EYK L + EGF+

Sbjct: 42 KLEISSAISEGAMAFVREYKVISLFIAFMAVLIVLLLDNPGSEGFND----- 90

Query: 135

TCKPALATAAFSTIAFVLGAVTSVLGFLGMKIATYANARTTLEARKGVGKAFIVAFRSG 194

++ IAFV GA+ S +SGF+GMKIAT N RT A+ + KAF VAF SG

Sbjct: 91 -----GIYTAIAFVSGALISCISGFIGMKIATAGNVRTAEAAKSSMAKAFRVAFDG 142

Query: 195 AVMGFLLAASGLLVLYITINVFK-

IYYGDDWEGLFEAITGYGLGGSSMALFGRVGGGIYT 253

AVMGF L +L ++ VF +Y G + L E++ G+GLGGS++ALFGRVGGGIYT

Sbjct: 143

AVMGFGLVGLAILGMIVLFLVFTGMYPGVEKHFLMESLAGFGLGSSAVALFGRVGGGIYT 202

Query: 254

KAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAEASCAALVV 313

KAADVGADLVGK+E+ IPEDDPRNPA IADNVGDNVGD+AGMG+DLFGS AEA+CAALV+

Sbjct: 203

KAADVGADLVGKVEKGIPEDDPRNPATIANVGDVAGMGADLFGSCAEATCAALVI 262

Query: 314 ASISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEIEPALKNQLIIST
373

++S ++ A+ YPLLIS+ GI ++T+ A +K +E ALK QL +ST

Sbjct: 263 GATAS-ALSGSVDALLYPLLISAFGIPASILTSFLA----RVKEDGNVESALKVQLWVST
317

Query: 374

VIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKWQLFLCVCVGLWAGLIIGFVTEYYTSNA 433

+++ + V+ + SF I K + W +++ + VGL++G+ IG VTEYYTS++

Sbjct: 318 LLVAGIMYFVTKTFMVDSFEI----AGKTITKWDVYISMVGLFSGMFIGIVTEYYTSHS
373

Query: 434

YSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXMYGVAVAALGM 493

Y PV++VA++ TGAATN+I+GL+LGY MYG+A+AALGM

Sbjct: 374 YKPVREVAEASNTGAATNIIYGLSLGYHSSVIPVILLVITIVTANLLAGMYGIAIAALGM
433

Query: 494

LSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIGKGFAIGSAA 553

+STIA GL IDAYGP+SDNAGGIAEMA + +R+RTD LDAAGNTTAAIGKGFAIGSAA

Sbjct: 434 ISTIAIGLTIDAYGPVSDNAGGIAEMAELGKEVRDRTDTLDAAGNTTAAIGKGFAIGSAA
493

Query: 554

LVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTMKSVGSAALKMVVEEV 613

L SLALF AF++R +++VL +V GL+ GAMLP+ F+AMTMKSVG AA+ MVVEEV

Sbjct: 494

LTSLALFAAFITRTHHTTSLEVLNAEVFGGLMFGAMLPFLFTAMTMKSVGKAAVDMVVEEV 553

Query: 614

RQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFFGVETLSGVL 673

+QF IPG+MEG KPDY CV IST A+++EMI PG LV+LTP++VG+ FGV+TL+GVL

Sbjct: 554 KQFKEIPGIMEGKNKPDYKRCVDISTSAAALREMILPGLLVLLTPILVGYLFGVKTLAGVL
613

Query: 674

AGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHKAAVIGDTIGDPL 733

AG+LV+GV +AISA+N+GG WDNAKKYIE K G KGS+ HKAAV+GDT+GDP

Sbjct: 614 AGALVAGVVLISAANSAGGGWDNAKKYIE-----KKAGGKGSQDQHKAAVVGDTVGDPPF
666

Query: 734 KDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

KDTSGPS+NILIKLMA+ SLVFA FF GG++FK F

Sbjct: 667 KDTSGPSINILIKLMAITSLVFAEFFVQQGGLIFKIF 703

☐ [>gi|13661740|gb|AAK38077.1|](#) H+-translocating inorganic pyrophosphatase TVP1

[*Toxoplasma gondii*]

Length = 816

Score = 611 bits (1576), Expect = e-173

Identities = 375/766 (48%), Positives = 480/766 (62%), Gaps = 61/766 (7%)

Query: 12 TEILVPICAVIGIAFSLFQWYVVSrvKLTSDLXXXXXXXXXXXXXXXXXXDYLIEEEGVND
71

T L + + ++IG+ +++++ + VS++++ L D L E G N

Sbjct: 83 TTCLLLLPSIIGLFWAVYEAWKVSKIQMDGPLGDDNKRLT-----DPLYLEMSG-NI 133

Query: 72

QSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXXLGsVEGFSTDNKPCTYD 131

Q + I I++GA +FL E+KY +G

Sbjct: 134 QQQLNMMKSISRciADGAVTFLTQEFKYMAVYIVVFSSILGIFVGI----- 179

Query: 132

TTRTCKPALATAAFSTIAFVLGAVTSVLsgFLGMKIATYANARTTLEARKGVGKAFIVAF 191

P +A AFVLGA+TS+L GF+GMKIA Y+N RT EA +G+ F VA

Sbjct: 180 -----PTMA-----AFVLGALTSILCGFVGMKIAVYSNVRTCHEAWMELGRGFQVAL 226

Query: 192 RSGAVMGFLLAASGLLVLYITINVFKI--YYG---DDWEGLFEAITGYGLGGSSMALFGR
246

+G+VMGF L + G L L I++++ +G +D LFEA+ GYGLGGSS+ALF R

Sbjct: 227

TAGSVMGFALVSLGCLTLVAILLYRLPSLFGTNPEDQRALFEAVAGYGLGGSSIALFAR 286

Query: 247

VGGGIYTKAADVGADLVGKIERNIPEDDPRNPaviADNVGDNVGDIAGMGSDLFGSYAEA 306

VGGGIYTKAADVGADL GK E + EDDPRNPA IADNVGDNVGD+AGMG+DLFGS AEA

Sbjct: 287

VGGGIYTKAADVGADLSGKNEYGMSEDDPRNPACIADNVGDNVGDVAGMGADLFGSLAEA 346

Query: 307 SCAALVVASIS-----SFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLV 358

SCA LV+A S G+ H + + + +P+LISS GI + T + F + +

Sbjct: 347

SCAGLVIAGASIATSASGGPQGLAHSWSGLMFPVLISSTGIFTGIFTVVLVRACFSVRCY 406

Query: 359

KEIEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWA 418

+IE ALK + IST + + + +S+ LP+ F + G Q W +CV +GLWA

Sbjct: 407 DDIEKALKWVMFISTGLEMPVLILLSYFFLPSEFLLD--
GCQGTAWWWHAAVCVVLGLWA 464

Query: 419

GLIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXX 478

GL IG+VTEYYTS++Y PV++++ + AAT +I+GLALGY

Sbjct: 465 GLAIGYVTEYYTSHSYFPVREISQTQIVSAATGIIYGLALGYSSTVPIICLGVTILVSH
524

Query: 479

XXXXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGN 538

MYG+A+AALGMLST+ GL ID YGPISDNAGGIAEMAG+ +R RTDALDAAGN

Sbjct: 525

TLCGMYGIALAALGMLSTLTMGLMIDGYGPISDNAGGIAEMAGLGPEVRSRTDALDAAGN 584

Query: 539

TTAAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTM 598

TTAA+GKG+AIGSAALVSLALFGAF RA I VDL P GLL GAM+PY FSAMTM

Sbjct: 585

TTAAVGKGYAIGSAALVSLALFGAFTVRAHITAVDVLDPWTFTGLLFGAMMPYAFSAMTM 644

Query: 599

KSVGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPL 658

KSVG AA MV+E +QF P +++G +P Y C++IST AS+ EMI PG LV+ P+

Sbjct: 645 KSVGIAASDMVQECLQQF---PLIIQGNI EPQYKRCIEISTRASLHEMIAPGALVICAPV
701

Query: 659 IVGFFFGVETLSGVLGSLVSGVQIAISASNTGGAWDNAKKYIEAGV--

SEHAKSLGPKG 716

G FG +G+LAG+LVSG+Q+AISAS +G AWDNAKKYIE+G ++H KG

Sbjct: 702 AAGMMFGKNCTAGLLAGALVSGIQLAISASTSGSAWDNAKKYIESGALGADHG-----
KG 756

Query: 717 SEPHKAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATH 762

S+ HK AV GDT+GDPLKDTSGPSLNILIKL A+ SLVF F A H

Sbjct: 757 SQAHKNAV TGDTVGDPLKDTSGPSLNILIKLSAII SLVFGAFIAEH 802

☐ >gj13661738|gb|AAK38076.1| H+-translocating inorganic pyrophosphatase TVP1
[Toxoplasma gondii]
Length = 816

Score = 610 bits (1573), Expect = e-173
Identities = 376/766 (49%), Positives = 479/766 (62%), Gaps = 61/766 (7%)

Query: 12 TEILVPICAVIGIAFSLFQWYVVSRLKLTSDLXXXXXXXXXXXXXXXXXXDYLIEEEGVND
71

T L + + + IG + + + + + + VS + + + + L D L E G N

Sbjct: 83 TTCLLLLPSIIGLFWAVYEAWKVSKIQMDGPLGDDNKRLT-----DPLYLEMSG-NI 133

Query: 72

QSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXXXLGSVEGFSTDNKPCTYD 131

Q + I I + + GA + FL E + KY LG G T

Sbjct: 134 QQQLNMMKSISRCIADGAVTFLTQEFKYMAVYIVVFSSI----LGIFVGIRT----- 181

Query: 132

TTRTCKPALATAAFSTIAFVLGAVTSVLGFLGMKIATYANARTTLEARKGVGKAFIVAF 191

AFVLGA + TS + L GF + GMKIA Y + N RT EA + G + F VA

Sbjct: 182 -----MAAFVLGALTSILCGFVGMKIAVYSNVRTCHEAWMELGRGFQVAL 226

Query: 192 RSGAVMGFLLAASGLLVLYITINVFKI--YYG---DDWEGLFEAITGYGLGGSSMALFGR
246

+G + VMGF L + G L L I + + + + +G +D LFEA + GYGLGGSS + ALF R

Sbjct: 227

TAGSVMGFALVSLGCLTLVAIILLYRLPSLFGTNPEDQRALFEAVAGYGLGGSSIALFAR 286

Query: 247

VGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAEA 306

VGGGIYTKAADVGADL GK E + EDDPRNPA IADNVGDNVGD + AGMG + DLFGS AEA

Sbjct: 287

VGGGIYTKAADVGADLSGKNEYGMSEDDPRNPACIADNVGDNVGDVAGMGADLFGSLAEA 346

Query: 307 SCAALVVASIS-----SFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLV 358

SCA LV+A S G+H+++ +P+LISS GI +T+ F++

Sbjct: 347

SCAGLVIAGASIATSASGGPQGLAHSWSGLMFPVLISSTGIFTGIFTVVLVRACFSVRCY 406

Query: 359

KEIEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWA 418

+IE ALK +IST+ +++S+ LP+F+ G Q W +CV+GLWA

Sbjct: 407 DDIEKALKWVMFISTGLEMPVLILLSYFFLPSEFLD--

GCQGTTAWWHAAVCVVLGLWA 464

Query: 419

GLIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXX 478

GL IG+VTEYYTS++Y PV++++ + AAT +I+GLALGY

Sbjct: 465 GLAIGYVTEYYTSHSYFPVREISQTQIVSAATGIIYGLALGYSSTVPIICLGVTLVSH
524

Query: 479

XXXXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGN 538

MYG+A+AALGMLST+ GL ID YGPISDNAGGIAEMAG+ +R RTDALDAAGN

Sbjct: 525

TLCGMYGIALAALGMLSTLTMGLMIDGYGPISDNAGGIAEMAGLGPEVRSRTDALDAAGN 584

Query: 539

TTAAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMTM 598

TTAA+GKG+AIGSAALVSLALFGAF RA I VDVL P GLL GAM+PY FSAMTM

Sbjct: 585

TTAAVGKGYAIGSAALVSLALFGAFTVRAHITAVDVLDPWFTTGLLFGAMMPYA FSAMTM 644

Query: 599

KSVGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPL 658

KSVG AA MV+E +QF P+++G +P Y C++IST AS+ EMI PG LV+ P+

Sbjct: 645 KSVGIAASDMVQECLQQF---PLIIQGNIEPQYKRCIEISTRASLHEMIAPGALVICAPV
701

Query: 659 IVGFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGV--

SEHAKSLGPKG 716

G FG +G+LAG+LVSG+Q+AISAS +G AWDNAKKYIE+G ++H KG
Sbjct: 702 AAGMMFGKNCTAGLLAGALVSGIQLAISASTSGSAWDNAKKYIESGALGADHG-----
KG 756

Query: 717 SEPHKAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATH 762
S+ HK AV GDT+GDPLKDTSGPSLNILIKL A+ SLVF F A H
Sbjct: 757 SQAHKNAVTVGDTVGDPLKDTSGPSLNILIKLSAISLVFGAFIAEH 802

☐ >gi|23509763|ref|NP_702430.1| V-type H(+)-translocating pyrophosphatase, putative
[Plasmodium
falciparum 3D7]
gi|23497614|gb|AAN37154.1| V-type H(+)-translocating pyrophosphatase, putative
[Plasmodium
falciparum 3D7]
Length = 717

Score = 585 bits (1507), Expect = e-165
Identities = 346/696 (49%), Positives = 450/696 (64%), Gaps = 47/696 (6%)

Query: 75
VAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXXXXLSVEGFSTDNKPCTYDTTR 134
V K E I + I + GA +FL E++Y + S
Sbjct: 48 VEKMKEIASYIAVGANAFLKKEFQYLAVFIIVFSILLGFFVNS----- 90

Query: 135
TCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVGKAFIVAFRSG 194
F+ ++FVLG +TS+L G++GMKIA YAN RTT E K + K F V +G
Sbjct: 91 -----FTAVSFVLGCLTSILCGYIGMKIAYVANVRTTNETWKS LDKGFQVTLNAG 140

Query: 195 AVMGFLLAASGLLVLYITINVFKIYYGDDW---
EGLFEAITGYGLGGSSMALFGRVGGGI 251
VMGF L + G++ L + I V+K Y + +++ I G+GLGGSS+ALF RVGGGI
Sbjct: 141 TVMGFSLVSFGIIALGLLIFVYKTYVFKNTIPDNQIYKIIAGFGLGGSSIALFSRVGGGI
200

Query: 252

YTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDVGMGSDLFGSYAEASCAAL 311

YTKAADVGADL GK E IPEDD RNPA IADNVGDNVGD+AGMG+DLFGS AE+ CAAL

Sbjct: 201

YTKAADVGADLSGKNEYGIPEDDIRNPACIADNVGDNVGDVGMGADLFGSLAESLCAAL 260

Query: 312 VVAS----ISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEIEPALKN 367

V+ S | + F + +PLL S ++ +IT T +I K++E +LK

Sbjct: 261 VIGSSVISIGEGSPGNAFHCLFPLLFVSFSVICSMITFYIITYSVKINDKKDVEKSLKY

320

Query: 368 QLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKWQLFLCVCVGLWAGLIIGFVTE

427

L++STV+ ++I ++V P+ + + K+ W++ + VGLW+GLIIGF TE

Sbjct: 321 LLLLSTVLQSLAILAIGYVCFPS---LVKYNYLKDIHRWKIIVPALVGLWSGLIIGFTTE 377

Query: 428

YYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXXMYGVA 487

+YTS ++SPVQ++A ++ AAT +I+GL+LGYK +YG+A

Sbjct: 378 FYTSYSFSPVQEIAHTQKVSAAATGIIYGLSLGYKSTFIPIICLSATLGISYGLCDIYGIA

437

Query: 488

VAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIGKGF 547

+AA+GMLST+ L IDAYGPISDNAGGIAEMAG+ +RERTD LDAAGNTTAAIGKGF

Sbjct: 438 LAAVGMLSTLCICLTIDAYGPISDNAGGIAEMAGLPSEVRERTDILDAAGNTTAAIGKGF

497

Query: 548

AIGSAALVSLALFGAFVSRAGIHTVDVLTTPKVIIGLLVGAMLPYWFSAMTMKSVGSAALK 607

AIGSAALV+ ALFGA+ S A + V++L VIIGLL+GAMLPY FSA+TMKSV AA

Sbjct: 498 AIGSAALVAFALFGAYASSANLRHVNILNSWWIIGLLIGAMLPYLFALTMTKSVAIAANS

557

Query: 608

MVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFFGVE 667

++ E QF P ++EG KPDY C+KISTDAS+++MI PG + + +PLI+G G
Sbjct: 558 VLNECLEQF---PLILEGKQKPDYKCIKISTDASLRQMIVPGLISVFSPLIIGMLMGKY
614

Query: 668 TLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGV--
SEHAksLGPkGSEPHKAavi 725

+G+L G ++SG+Q+A S++N+GGAWDNAKKYIE+G EH KGS HK +VI
Sbjct: 615 ATAGLLIGIILSGIQLAFSSTNSGGAWDNAKKYIESGALGKEHC-----KGSNAHKNSVI
669

Query: 726 GDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFAT 761

GDT+GDPLKDTSGPSLNILIKL A+ SLVFA AT
Sbjct: 670 GDTVGDPLKDTSGPSLNILIKLSAITSLVFANVIAT 705

☐ >gi|4324984|gb|AAD17215.1| proton-pumping vacuolar pyrophosphatase; plant vacuolar
pyrophosphatase homolog; PVP [Plasmodium falciparum]
Length = 717

Score = 585 bits (1507), Expect = e-165
Identities = 346/696 (49%), Positives = 450/696 (64%), Gaps = 47/696 (6%)

Query: 75

VAKCAEIQTaiseGATSFLFTEYKYXXXXXXXXXXXXXXXXXlGSVEGFSTDnKPCTYDTTR 134

V K EI + I + GA + FL E ++ Y + S
Sbjct: 48 VEKMKEIASYIAVGANAFLKKEFQYLAVFIIVFSILLGFFVNS----- 90

Query: 135

TCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVGKAFIVAFRSG 194

F + ++FVLG + TS + L G ++ GMKIA YAN RTT E K + K F V + G
Sbjct: 91 -----FTAVSFVLGCLTSILCGYIGMKIAYANVRTTNETWKS LDKGFQVTLNAG 140

Query: 195 AVMGFLLAASGLLVLYITINVFKIYYGDDW---

EGLFEAITGYGLGGSSMALFGRVGGGI 251
VMGF L + G ++ L + I V + K Y + +++ I G + GLGGSS + ALF RVGGGI

Sbjct: 141 TVMGFSLVSFGIIALGLLIFVYKTYVFKNTIPDNQIYKIIAGFGLGGSSIALFSRVGGI
200

Query: 252

YTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDVGMGSDLFSGSYAEASCAAL 311
YTKAADVGADL GK E IPEDD RNPA IADNVGDNVGD+AGMG+DLFGS AE+ CAAL

Sbjct: 201

YTKAADVGADLSGKNEYGIPEDDIRNPACIADNVGDNVGDVGMGADLFGLAESLCAAL 260

Query: 312 VVAS---ISSFGINHFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEIEPALKN 367

V+ S I + F ++PLL S ++ +IT T +I K++E +LK

Sbjct: 261 VIGSSVISIGEGSPGNAFHCILFPLLFVSFVCSMITFYIITYSVKINDKKDVEKSLKY
320

Query: 368 QLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKWQLFLCVCVGLWAGLIIGFVTE
427

L++STV+ ++I ++V P+ + + K+ W++ + VGLW+GLIIGF TE

Sbjct: 321 LLLLSTVLQSLAILAIGYVCFPS---LVKYNLYKDIHRWKIIVPALVGLWSGLIIGFTTE 377

Query: 428

YYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXXMYGVA 487
+YTS ++SPVQ++A ++ AAT +I+GL+LGYK +YG+A

Sbjct: 378 FYTSYSFSPVQEIAHTQKVSAATGIIYGLSLGYKSTFIPICLSATLGISYGLCDIYGIA
437

Query: 488

VAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIGKGF 547
+AA+GMLST+ L IDAYGPISDNAGGIAEMAG+ +RERTD LDAAGNTTAAIGKGF

Sbjct: 438 LAAVGMLSTLCICLTIDAYGPISDNAGGIAEMAGLPSEVRERTDILDAAGNTTAAIGKGF
497

Query: 548

AIGSAALVSLALFGAFVSRAGIHTVDVLTTPKVIIGLLVGAMLPYWFSAMTMKSVGSAALK 607
AIGSAALV+ ALFGA+ S A + V++L VIIGLL+GAMLPY FSA+TMKSV AA

Sbjct: 498 AIGSAALVAFALFGAYASSANLRHVNILNSWVIIGLLIGAMLPYLFSAITMKSVIAAANS
557

Query: 608

MVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFFGVE 667

++ E QF P ++EG KPDY C+KISTDAS+++MI PG ++ +PLI+G G

Sbjct: 558 VLNECLEQF---PLILEGKQKPDYEKCIKISTDASLRQMIVPGLISVFSPLIIGMLMGKY
614

Query: 668 TLSGVLÄGSLVSGVQIAISASNTGGAWDNAKKYIEAGV--

SEHAksLGPkGSEPHKAAVI 725


+G+L G ++SG+Q+A S++N+GGAWDNAKKYIE+G EH KGS HK +VI

Sbjct: 615 ATAGLLIGIILSGIQLAFSSTNSGGAWDNAKKYIESGALGKEHC-----KGSNAHKNSVI
669

Query: 726 GDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFAT 761

GDT+GDPLKDTSGPSLNILIKL A+ SLVFA AT

Sbjct: 670 GDTVGDPLKDTSGPSLNILIKLSAITS LVFANVIAT 705

 [>gi|23483521|gb|EAA19163.1|](#) V-type H(+)-translocating pyrophosphatase [Plasmodium
yoelii

yoelii]

Length = 716

Score = 582 bits (1501), Expect = e-165

Identities = 356/767 (46%), Positives = 471/767 (61%), Gaps = 73/767 (9%)

Query: 7 LPELWTEILVPICAVIGIAFSLFQWYVVSrvKLTSDLXXXXXXXXXXXXXXXXXXDYLIEEE

66

+ EL+ I P V+G+ FS++ +SR++ + D L + E

Sbjct: 1 MKELYCIIFGP--PVLGLLFSVIECISIRIHIGAS-----DDKLDKVE 42

Query: 67

EGVNDQSVVAKCAEIQTASEGAT\$FLFTEYKYXXXXXXXXXXXXXXXXXLGSVEGFSTDNK 126

G Q++ K EI + ISEGA SFL EY+Y +

Sbjct: 43 NG---QAKIEKMKEIASYISEGANSFLSKEYQYLIVFMILFSGLLSWFINY----- 90

Query: 127

PCTYDTRTCKPALATAAFSTIAFVLGAVTSVLGFLGMKIATYANARTTLEARKGVGKA 186

++ I+F +G +TS++ G++GMKIA YAN RTT E K + K

Sbjct: 91 -----YTAISFAIGCITSIIICGYIGMKIAVYANVRTTSETWKSLDKG 132

Query: 187 FIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYG-

DDWEGLFEAITGYGLGGSSMALFG 245

F V +G VMGF L + ++ L I +K + D L++A I G+GLGGSS+ALF

Sbjct: 133 FKVTNLNAGTVMGFSVLVLSIISLGALIFAYKAQFQFSDDPALYKAIAGFGLGGSSIALFS
192

Query: 246

RVGGGIYTKAADVGADLVGKIERNIPEDDPRNPVADNVGDNVGDIAGMGSDLFGSYAE 305

RVGGGIYTKAADVGADL GK E IPEDD RNPA IADNVGDNVGD+AGMG+DLFGS AE

Sbjct: 193

RVGGGIYTKAADVGADLSGKNEYGIPEDDIRNPACIADNVGDNVGDMAGMGADLFGSLAE 252

Query: 306 ASCAALVVAS-----ISSFGINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKL 357

+ CA+LV+ S + SF IN+ F +PL SS I+ ++T T +

Sbjct: 253 SLCASLVIGSSVLSPENMKSF DINYCFM---FPLFFSSASIISSMLTFFLVTKIVRVTG
309

Query: 358

VKEIEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLW 417

++E LK L IST+ ++I +V LP + + K +NW+++ VGLW

Sbjct: 310 KEGVERTLKYLLFISTIFQSLTIFVVGQYCLPP---VLVDVLKQIPNWKIIPALVGLW
366

Query: 418

AGLIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXX 477

+GLIIGF TE+YTS ++ PVQ++A++ + AAT +I+GL+LGYK

Sbjct: 367 SGLIIGFTTEFYTSYSFRPVQEIA NTQKISAATGIYGLSLGYKSTFIPIICLSGALGIS 426

Query: 478

XXXXXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAG 537

+YGVA+AA+GMLST+ L IDAYGPISDNAGGIAEMAG+ +RE+TD LDAAG

Sbjct: 427

YVFCEVYGVALAAVGMLSTLCICLTIDAYGPISDNAGGIAEMAGLPSEVREKTDILDAAG 486

Query: 538

NTTAAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFSAMT 597

NTTAAIGKGFAIGSAALV+ ALFGA+ S A + V++L P VIIGLL+G+MLPY FSA+T

Sbjct: 487 NTTAAIGKGFAIGSAALVAFALFGAYASSAKVRHVNILNPWVIIGLLIGSMLPYLFSALT
546

Query: 598

MKSVGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTP 657

MKSV AA ++ E QF P ++ KPDY C+KISTDAS+++MI PG + + P

Sbjct: 547 MKSVAIAANSVLNECLEQF---PLILANKQKPDYDKCIKISTDASLRQMILPGLISVTFP
603

Query: 658 LIVGFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGV--

SEHA KSLGPK 715

LI+G G +G+L G ++SG+Q+A S++N+GGAWDNAKKYIE+G ++H K

Sbjct: 604 LIIGMLMGKYATAGLLIGIILSGIQLAFSSTNSGGAWDNAKKYIESGALGTDHC-----K
658

Query: 716 GSEPHKAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATH 762

GS HK +VIGDT+GDPLKDTSGPS+NILIKL A+ SLVFA + H

Sbjct: 659 GSNAHKNSVIGDTVGDPLKDTSGPSINILIKLSAITSLVFAGLISNH 705

☐ [>gi|14149007|emb|CAC39165.1|](#) vacuolar-type H⁺-pyrophosphatase [*Lycopersicon
esculentum*]

Length = 356

Score = 570 bits (1468), Expect = e-161

Identities = 317/356 (89%), Positives = 323/356 (90%)

Query: 415

GLWAGLIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXX 474

GLWAGLIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 1 GLWAGLIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKS VIIPIFAIAISI 60

Query: 475

XXXXXXXXXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALD 534

MYG+AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALD

Sbjct: 61

FVSFSFAAMYGIABAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALD 120

Query: 535

AAGNTTAAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLT PKVIIGLLVGAMLPYWFS 594

AAGNTTAAIGKGFAIGSAALVSLALFGAFVSRA I TVDVLT PKV IGLLVGAMLPYWFS

Sbjct: 121

AAGNTTAAIGKGFAIGSAALVSLALFGAFVSRAAISTVDVLT PKVFIGLLVGAMLPYWFS 180

Query: 595

AMTMKSVGSAALKMVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVM 654

AMTMKSVGSAALKMVEEVR QFNTIPGLME TAKPDYATCVKI TDASIKEMIPPG LVM

Sbjct: 181

AMTMKSVGSAALKMVEEVRXQFNTIPGLMERTAKPDYATCVKIFTDASIKEMIPPGALVM 240

Query: 655

LTPLIVGFFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGP 714

LTPLIVG FGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAG SEHA++LGP

Sbjct: 241

LTPLIVGILFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGASEHARTLGP 300

Query: 715 KGSEPHKAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

KGS+ HKAAVIGDT+GDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGG+LKF F

Sbjct: 301 KGSDAHKAAVIGDTVGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGLLFKLF 356



>gi|28210139|ref|NP_781083.1| vacuolar-type H⁺-pyrophosphatase [Clostridium tetani E88]

gi|33301168|sp|Q898Q9|HPPA_CLOTE Pyrophosphate-energized proton pump

(Pyrophosphate-energized

inorganic pyrophosphatase) (H⁺-PPase) (Membrane-bound
proton-translocating pyrophosphatase)

gij28202575|gb|AAO35020.1| vacuolar-type H⁺-pyrophosphatase [Clostridium tetani E88]

Length = 673

Score = 513 bits (1320), Expect = e-144

Identities = 334/696 (47%), Positives = 426/696 (61%), Gaps = 72/696 (10%)

Query: 80

EIQTAISEGATSFLFTEYKYXXXXXXXXXXXXXXXXXLGSVEGFSTDNKPCTYDTRTCKPA 139

EI I +GA +FL TEYKY +G

Sbjct: 38 EIAGHIHDGAMAFLKTEYKYLTGFIVIVTVILAIFVG----- 74

Query: 140

LATAAFSTIAFVLGAVTSVLGFLGMKIATYANARTTLEARKGVGKAFIVAFRSGAVMGF 199

TAA F+LGA+ S+ +G+ GM +AT AN RT AR GKA +AF GAVMG

Sbjct: 75 WQTAA---CFILGAIFSIFAGYFGMNVATKANVRTAEARHSQGKALNIAFSGGAVMGM
130

Query: 200

LLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMALFGRVGGGIYTKAADVG 259

+ G++ +I +F G E +TG+GLG SS+ALF RVGGGIYTKAADVG

Sbjct: 131 SVVGLGVVGIGIMYYIFG-----GNMEFVTGFGLGASSIALFARVGGGIYTKAADVG
182

Query: 260

ADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAEASCAALVVASISSF 319

ADLVGK+E IPEDDPRNPAVIADNVGDNVGD+AGMG+DLF SY + +AL + ++

Sbjct: 183 ADLVGKVEAGIPEDDPRNPAVIADNVGDNVGDVAGMGADLFESYVGSIIISALT LGTV--
- 239

Query: 320 GINHDTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEIEPALKNQLIISTVIMTVG
379

+ + + +PL++SS+G|+ +I LF+ K+ + AL I +I+ V

Sbjct: 240 -VYANKEGVMFPLILSSIGIVASIIGILFSRK----SKAKDPQKALNTGTYIGGIIVIVS 294

Query: 380

IAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGLIIGFVTEYYTSNAYSPVQD 439

AI+S TIF N + F V GL G+IIG +TE YTS+AYS VQ

Sbjct: 295 AAILS-----NTIFG-----NLKAFFAVASGLVVGMIIGKITEMYTSDAYSSVQK 339

Query: 440 VADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXX-----MYGVAVAAL
491

+A+ TG AT +I GLA+G +YG+++AA+

Sbjct: 340 IANQSETGPATTIISGLAVGMYSTLWPIVLISIGVLVSFFVMGGGSNAMVGLYGISLA
399

Query: 492

GMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTAAIGKGFAIGS 551

GMLST +A+DAYGPI+DNAGGIAEM+ + H +RE TD LD+ GNTTAAIGKGFAIGS

Sbjct: 400

GMLSTTGLTVAVDAYGPIADNAGGIAEMSELPHEVREITDKLDSVGNTTAAIGKGFAIGS 459

Query: 552

AALVSLALFGAFVSRAGIHTVDVLT PKV IIGLLVGAMLPYWFSAMTMKSVGSAALKMVEE 611

AAL +L+LF ++ + ++D+L ++GL +GAMLP+ F A+TM+SVG AA +M+EE

Sbjct: 460 AALTALSLFASYAQATELESIDILNTVTLVGLFIGAMLPFLFGALTMESVGKAANEMIEE
519

Query: 612

VRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFFGVETLSG 671

VRRQF TIPG+MEG A PDY CV IST A+I+EMI PG L ++ P+ +G G E L G

Sbjct: 520

VRRQFKTIPGIMEGKATPDYKKCVDISTAAAIEMILPGVLAIVVPVAMGLLLGKEALGG 579

Query: 672

VLGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHKAAVIGDTIGD 731

+LAG+LVSGV +I SN GGAWDNAKKYIE G G KGSE HKA AV+GDT+GD

Sbjct: 580 LLAGALVSGVLVGILMSNAGGAWDNAKKYIEGGAH-----
GGKGSEAHKAAVVGDTVGD 633

Query: 732 PLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILF 767

P KDTSGPS+NILIKLM + SLVFAP +GGIL

Sbjct: 634 PFKDTSGPSMNILIKLMTIVSLVFAPVVLQYGGILL 669

--
-

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF excluding environmental samples
Posted date: Jun 21, 2004 12:17 AM
Number of letters in database: 619,299,334
Number of sequences in database: 1,865,463

Lambda K H
0.322 0.138 0.405

Gapped

Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 166,000,056
Number of Sequences: 1865463
Number of extensions: 6612265
Number of successful extensions: 18550
Number of sequences better than 10.0: 41
Number of HSP's better than 10.0 without gapping: 34
Number of HSP's successfully gapped in prelim test: 7
Number of HSP's that attempted gapping in prelim test: 18354
Number of HSP's gapped (non-prelim): 60
length of query: 770
length of database: 619,299,334
effective HSP length: 133

effective length of query: 637

effective length of database: 371,192,755

effective search space: 236449784935

effective search space used: 236449784935

T: 11

A: 40

X1: 16 (7.4 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.9 bits)

S2: 78 (34.7 bits)

EXHIBIT B



May 17, 2004 11:45AM

FEBS 22076

No. 2952 P. 1

FEBS Letters 452 (1999) 121-127

Minireview

H⁺-proton-pumping inorganic pyrophosphatase: a tightly membrane-bound family

Margareta Baltscheffsky*, Anders Schultz, Herrick Baltscheffsky

Department of Biochemistry, Arrhenius Laboratories, Stockholm University, S-106 91 Stockholm, Sweden

Received 11 March 1999; received in revised form 30 March 1999

6354

Abstract The earliest known H⁺-proton-pumping inorganic pyrophosphatase, the integrally membrane-bound H⁺-proton-pumping inorganic pyrophosphate synthase from *Rhodospirillum rubrum*, is still the only alternative to H⁺-ATP synthase in biological electron transport phosphorylation. Cloning of several higher plant vacuolar H⁺-proton-pumping inorganic pyrophosphatase genes has led to the recognition that the corresponding proteins form a family of extremely similar proton-pumping enzymes. The bacterial H⁺-proton-pumping inorganic pyrophosphate synthase and two algal vacuolar H⁺-proton-pumping inorganic pyrophosphatases are homologous with this family, as deduced from their cloned genes. The prokaryotic and algal homologues differ more than the H⁺-proton-pumping inorganic pyrophosphatases from higher plants, facilitating recognition of functionally significant entities. Primary structures of H⁺-proton-pumping inorganic pyrophosphatases are reviewed and compared with H⁺-ATPases and soluble proton-pumping inorganic pyrophosphatases.

© 1999 Federation of European Biochemical Societies.

Key words: H⁺-proton-pumping inorganic pyrophosphatase; H⁺-proton-pumping inorganic pyrophosphate synthase; H⁺-ATPase; H⁺-ATP synthase; Amino acid sequence; Evolution; Enzyme family

1. Introduction

Photophosphorylation of inorganic orthophosphate (Pi) to pyrophosphate (PPi), in chromatophores isolated from the photosynthetic, purple, non-sulfur bacterium *Rhodospirillum rubrum*, was discovered in 1966 [1] and found to be sensitive to uncouplers but uninhibited by oligomycin [2]. This light-induced formation of PPi, which provided a *raison d'être* for the tightly membrane-bound uncoupler stimulated, inorganic pyrophosphatase (PPase) activity in chromatophores [3,4], is still the only known alternative to ATP formation in biological electron transport phosphorylation. In isolated chromatophores, PPi was used to drive several energy requiring reactions [5-8]. Proton movement, which was induced by light in chromatophores [9], was shown by addition of PPi in the dark to be linked also to the PPase [10], thus showing it to be a

H⁺-PPase (H⁺-PPi synthase, compare H⁺-F₀F₁ATPase, H⁺-F₀F₁ATP synthase).

A membrane-bound PPase activity was found in 1975 in homogenates from higher plants [11] and was later localized to plant vacuoles [12]. In plants, the vacuoles contain two enzymes for acidifying the interior of the vacuole, the well known V-ATPase and the V-PPase (V for vacuolar).

Nine amino acid sequences of plant V-PPases have been solved and shown to form a distinct protein family [13-21]. Two are from green algae and have been published very recently [20,21]. The higher plant sequences show identities of more than 85% [18]. From bacteria, the *R. rubrum* H⁺-PPase (PPi synthase) sequence [22] belongs to the same family, as do two homologues which have emerged from genomics work with hyperthermophiles, namely the archaeon *Pyrococcus aerophilus* and the bacterium *Thermotoga maritima*.

H⁺-PPase activity has also been documented in several other membranes from higher plants [23-25], as well as in acidocalcisomes from the protozoan *Trypanosoma cruzi* [26] and the cell membrane of the chemotrophic anaerobic bacterium *Syntrophus gentianae* [27].

An excellent review [28] on pyrophosphate as an energy donor in plant cells discusses in great detail the possible interplay between ATP-linked and PPi-linked reactions. As several recent review articles [29-31] cover the eukaryotic H⁺-PPases, this minireview is somewhat focussed on the prokaryotic homologues. Emphasis is also on H⁺-PPases with a known primary structure and on comparison with both H⁺-ATPases and soluble PPases. X-ray structures at high resolution of crystals from soluble PPases from both pro- and eukaryotes have provided the background for most of the detailed knowledge about the structure and reaction mechanism, also in other PPases. Whereas the membrane-bound PPases are directly involved in bioenergetic reactions, soluble PPases have long been recognized to function in the hydrolysis of the PPi emerging as a byproduct from various ATP requiring biosyn-

```
CGCTCCCGCCGCGTGGTCTGCGAGCTCCCTTACCTTCCGCGCAGACCCCGCGCTCG
ATGTGGCTATTGATCGCGCGCGCGGTCTTCCCGCATTCCTCCGCTTACCGCCATTACGGGCG
GGATCGAAGCAATCACTGCTGCTATCTTTTCCTGCTAGCCGCGCCACTCGCGCGC
HAGIYLFVVAALAA
CTTGTTATGGCGCTCTCACCATCAAAACATCATGCGCGCTGATGCGGCGACCGCGGATGC
LCYGCALTIXTHAADAAGTARH
AAGGATTTCGCGCGCGCTGAGGAAGCGCGCGCGGTTCCTCATGCTCAGTCAAGACCAT
GCTISGAVQEGASAFLLNRQYXY
H
Alternative start
```

Fig. 1. The first 319 nucleotides from the N-terminal end of the clone RrPP4. The two identical Shine Dalgarno regions (GAG) and the two possible start codons (ATG and GTG, in bold script) are underlined. Corresponding amino acids for the two alternatives are given.

*Corresponding author. Fax: (46) (8) 153 679.
E-mail: meg@biokemi.su.se

Abbreviations: PPi, inorganic pyrophosphate; PPase, inorganic pyrophosphatase; ATP, adenosine triphosphate; ATPase, adenosine triphosphatase

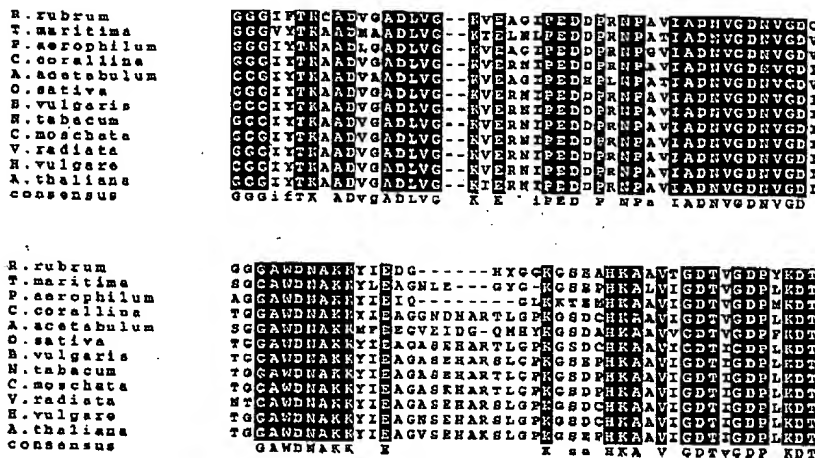


Fig. 3. Alignment with the parts of two loops between transmembrane segment 5-6 (above) and 15-16 (below) in H^+ -PPases, where the part of loop 5-6 contains the three motifs GGG, DVGADLVGK and DNVGDNVGD. Residues in black/gray boxes are identical/similar in all sequences. The consensus of similarities follows that of the first organism.

exception is the motif DX₇KXE [44] in the loop after transmembrane segment 5 which is similar to the active site motif EX₇KXE in soluble PPases [50]. Antibodies directed to this motif in *V. radiata* V-PPase were recently shown to strongly inhibit the hydrolytic and proton-pumping activity of membrane vesicles and the hydrolytic activity of the purified enzyme [51]. A specific chemical inhibitor for H^+ -PPases from both plants and photobacteria is aminomethylenediphosphate [52].

Amino acid sequences of algal V-PPases from *Acetabularia* [20] and *Chara corallina* [21] have very recently emerged. The *A. acetabulum* sequence shows approximately as many identities with the *R. rubrum* sequence as with the one from *A. thaliana* (see Fig. 2), whereas the *C. corallina* sequence is much more like that of *A. thaliana*. A possible link between vacuolar and bacterial H^+ -PPases is the new homologue from *A. thaliana*. It shows more sequence identities with the *R. rubrum* H^+ -PPase (40.1%) than with any of the vacuolar H^+ -PPases (33.4–37.2%). Furthermore, the homologue contains one of two cysteines of the putative active site loop of the *R. rubrum* H^+ -PPase. The substitution of E in the motif EYYT to K indicates that the homologue may no longer possess coupling activity.

4. Some further structural and evolutionary aspects

The amino acid sequences of the bacterial PPI synthase from *Rhodospirillum*, the homologue from *Thermotoga* and nine published vacuolar H^+ -PPases are shown in Fig. 2. Comparisons with hydrophobic plots show that identical (blackened) and similar (shadowed) residues are particularly abundant between transmembrane segments, in the loops 5, 11 and 15.

The homology between all membrane-bound H^+ -PPases has led to various questions, about common structural properties of functional significance and about evolution, both within these archaeal, bacterial, algal and higher plant en-

zymes and between this protein family and possibly related families, such as membrane-bound ATPases and soluble PPases.

4.1. Within the H^+ -PPase family

Attention is here first restricted to corresponding parts of two loops in the PPI synthase from *R. rubrum*. A 45 amino acid piece from the 57 amino acids in the putative active site loop 5 is compared with a similar part of loop 15, which may contain a duplicated and subsequently evolved segment of an ancestral version of loop 5. Three motifs of loop 5 are GGG, DVGADLVGK and DNVGDNVGD.

The first motif, the triglycyl sequence, occurs in all H^+ -PPase family members and may be expected to have the potential to provide, to the extent that other structural properties of the enzyme allow, an unusually high local conformational change capability. In the PPI synthase, uniquely, the loop 15, with the 'duplicated segment', contains a similarly positioned sequence of three glycyl residues, in contrast to just two or one in all other known H^+ -PPases (Fig. 3). In view of the conformational change mechanism of the ATP synthase function [53,54], one may ask the question if the fact that only the PPI synthase of the H^+ -PPase family may function physiologically in the PPI synthesis direction is related to this uniqueness. Notably, a GGG sequence has recently been used as a spacer to allow mimicking the swing of the lever arm of a myosin motor [55].

It should be pointed out that in the H^+ -PPI synthase, a mechanism of rotation in energy coupling, similar to that of ATP synthase [54], seems impossible since the H^+ translocation and the catalytic site are on the same subunit, as in P-type ATPases. The alternative phosphorylation system, generating PPI, thus would appear to utilize a fundamentally different coupling mechanism from that involved in the ATP synthesis.

Results from high resolution studies of crystals from soluble PPases [50] indicate that the second motif, DVGADLVGK,

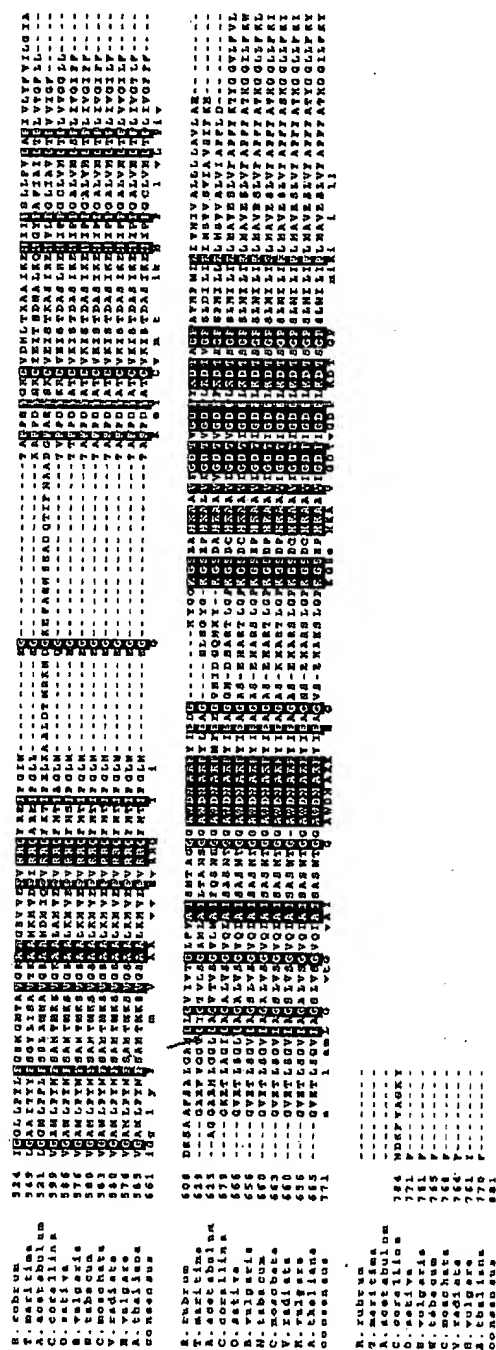


Fig. 2. Multiple sequence alignment with H⁺-PPase sequences from *R. rubrum*, the thermophilic bacterium *T. uaridus*, the unicellular algae *A. acetabulum*, the green algae *C. corallina* and the plants *Oryza sativa*, *Beta vulgaris*, *Nicotiana tabacum*, *Cucurbita maxima*, *Vigna radiata*, *Hordeum vulgare* and *A. thaliana*.

thetic reactions, thus facilitating the actual biosyntheses. The known PPase families are briefly described in Table 1.

2. The *R. rubrum* H⁺-PPi synthase and homologues from prokaryotes

A very tightly membrane-bound enzyme was found to be responsible for the PPase and the PPI synthase activity [4] in *R. rubrum*. The energetic capacity of PPI was further elucidated when it was possible to drive a reversed electron flow with the energy released by the hydrolysis of PPI [5,6], as well as to create a membrane potential [32–34] over both the chromatophore membrane and artificial membranes. It was also possible in chromatophores to drive the phosphorylation of ADP to ATP in the dark with PPI [8]. The 'cost' of PPI in this experiment was about eight per ATP synthesized, which leads to the question of the proton stoichiometry in PPI hydrolysis. Values obtained vary between 0.5 [10] and two H⁺ [35,36] per PPI hydrolyzed. Very interesting in this connection is that in plasma membrane vesicles from *S. gentianae* [27], the hydrolysis of one ATP yields three PPI and vice versa, three PPI yield one ATP, indicating a H⁺ stoichiometry of one for PPI hydrolysis. The isolated and purified enzyme could be reconstituted in artificial liposomes with a retained activity [37] and when co-incorporated with the complete F₀F₁ complex from *R. rubrum*, ATP synthesis driven by PPI hydrolysis was obtained also in the liposomes [38]. In the bacteria, the PPI synthase is situated in the plasma membrane with the same polarity as the ATP synthase, with the catalytic site towards the cytosol. PPI synthesis and ATP synthesis compete for the available proton gradient, at least in isolated chromatophores [39]. The rate of PPI synthesis, at a saturating light intensity, is 12–15% of the rate of ATP synthesis.

The enzyme is extremely hydrophobic, a property which has caused considerable difficulty in both the original isolation and the determination of the amino acid sequence. Several attempts have been made to make a direct analysis on the isolated and purified protein, all of which have failed, probably due to the high percentage of detergent necessary to keep it active in solution. The cloning and sequencing of the gene encoding the PPase left one problem unsolved. Two possibilities for the start codon of the gene appeared, separated by 126 bp, one yielding a deduced protein of 660 amino acids with a molecular mass of 67 453 [22], the other giving a structure with 702 amino acids with the molecular mass 71 609 (Fig. 1). The two bacterial H⁺-PPase homologues which both contain more than 700 amino acids are more similar to the longer version of the *R. rubrum* sequence. So is the suggested dimer structure of the *R. rubrum* PPI synthase with a molecular mass of 167.7 ± 30.7 kDa [40], as determined by radiation inactivation. A dimer has also been suggested based on ultrafiltration results [41]. Another argument favoring the 702 amino acid length is that there are only 15 predicted transmembrane segments in the 660 amino acid structure [22], whereas the 702 amino acid one has 16, as have all the other homologues in the H⁺-PPase family. No striking homology with the N-terminals of known H⁺-PPases is

Table 1
Known PPase families

Family	Members
1. Tightly membrane-bound H ⁺ -pumping PPases	a. Bacterial PPase b. Archaeal and bacterial homologues c. Vacuolar PPases
2. Earlier known family of soluble PPases	a. Cytoplasmic PPases (archaeal, bacterial and eukaryotic) b. Mitochondrial (and chloroplast?) PPases (probably soluble parts of H ⁺ pumps)
3. Recently found family of soluble PPases	a. Some archaeal and bacterial PPases

found, but a new homologue from the *Arabidopsis thaliana* genome (Vysotskaia, V.S. et al., GenBank, accession AC005679) shows a particular similarity to the *R. rubrum* sequence, both with respect to the complete protein and to the N-terminal part, unique to its longer version, which is used in this paper. A final conclusion about the actual start may have to await successful sequencing of the N-terminal part of the *R. rubrum* enzyme.

The *Rhodospirillum*, *Pyrobaculum* and *Thermotoga* sequences show only about 38–39% identities between themselves, which indicates that they are much more diverged from each other than the higher plant enzymes are. An intriguing question is whether the two prokaryotic H⁺-PPase homologues will be physiologically active and also capable as PPI synthases as those from *R. rubrum* and *R. viridis* [42].

3. H⁺-PPases in plant vacuoles

The main role of V-PPases seems to be to participate in the acidification of vacuoles. In tonoplasts from *Zea mays* L., PPI synthesis has been obtained in response to a H⁺-gradient created by ATP hydrolysis, as well as ATP synthesis in response to a PPI-generated H⁺-gradient [43]. The dependence of V-PPase activity on K⁺ ions [44] has led to a debated suggestion of V-PPase-mediated physiological transport of K⁺ ions into vacuoles [28]. Also, V-PPases probably occur as dimers *in vivo* [45].

The V-PPase from *Arabidopsis* has been heterologously expressed in yeast [46]. At least four V-PPases have been reconstituted in liposomes [47] with a retained activity. Site-directed mutation studies of *Arabidopsis* V-PPase expressed in yeast have revealed some amino acids of apparent functional importance [48]. E427, located on the cytosolic side immediately after the predicted transmembrane segment 9, is of particular interest since an E427Q mutant preferentially impairs H⁺ translocation over PPI hydrolysis and the E427D mutant enhances H⁺ translocation [48]. E427 is included in a motif, EYYT, present in all sequenced H⁺-PPases, except in *Pyrobaculum*, where it is the similar DYYT. D504 is also conserved in the H⁺-PPases and mutant D504N essentially, lacks both PPase activity and H⁺ translocation.

The first indicated family relationship between vacuolar and bacterial H⁺-PPases was found when antibodies directed against the V-PPase of *Vigna radiata* cross-reacted with the *R. rubrum* PPI synthase [49]. Both bacterial and vacuolar H⁺-PPases show few sequence similarities with soluble PPases. An

¹ Sequence data were obtained through early release from The Institute for Genomic Research at www.tigr.org and/or through NCBI at www.ncbi.nlm.nih.gov.

To introduce
unit in *A. thaliana*

Fig. 3. Alignment with the parts of two loops between transmembrane segment 5-6 (above) and 15-16 (below) in H⁺-PPases, where the part of loop 5-6 contains the three motifs GGG, DVGADLVGK and DNVGDNYGD. Residues in black/gray boxes are identical/similar in all sequences. The consensus of similarities follows that of the first organism.

zymes and between this protein family and possibly related families, such as membrane-bound ATPases and soluble PPases.

Attention is here first restricted to corresponding parts of two loops in the PPI synthase from *R. rubrum*. A 45 amino acid piece from the 57 amino acids in the putative active site loop 5 is compared with a similar part of loop 15, which may contain a duplicated and subsequently evolved segment of an ancestral version of loop 5. Three motifs of loop 5 are GGG, DVGADLVGK and DNVGDNYGD

It should be pointed out that in the H^+ -PPI synthase, a mechanism of rotation in energy coupling, similar to that of ATP synthase [54], seems impossible since the H^+ translocation and the catalytic site are on the same subunit, as in P-type ATPases. The alternative phosphorylation system, generating PPI, thus would appear to utilize a fundamentally different coupling mechanism from that involved in the ATP synthesis.

Results from high resolution studies of crystals from soluble PPases [50] indicate that the second motif, DVGADLVGK,

The amino acid sequences of the bacterial PPi synthase from *Rhodospirillum*, the homologue from *Thermotoga* and nine published vacuolar H⁺-PPases are shown in Fig. 2. Comparisons with hydrophobic plots show that identical (blackened) and similar (shadowed) residues are particularly abundant between transmembrane segments, in the loops 5, 11 and 15.

The homology between all membrane-bound H^+ -PPases has led to various questions, about common structural properties of functional significance and about evolution, both within these archaeal, bacterial, algal and higher plant en-

EXHIBIT C

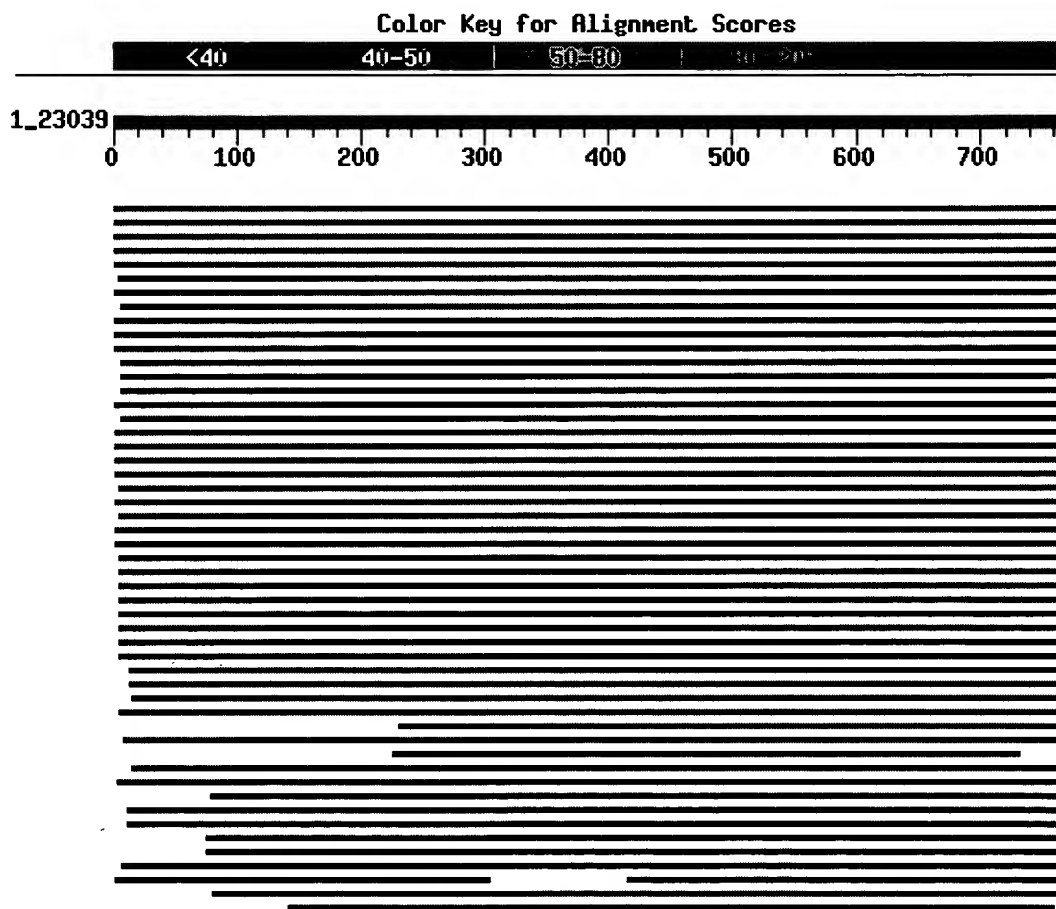


BLASTP 2.2.9 [May-01-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

Distribution of 100 Blast Hits on the Query Sequence



Plants (mono and dicots)	% Identity at the amino acid level
<i>Lycopersicon esculentum</i> (Tomato)	89
barley	81
<i>Oryza sativa</i> (rice)	82
<i>Nicotiana tabacum</i> (common tobacco)	84
<i>Prunus persica</i> (peach)	84
<i>Cucurbita moschata</i> (butter-nut squash)	83
<i>Beta vulgaris</i> (sugar beet)	84
<i>Triticum aestivum</i> (wheat)	80
<i>Vitis vinifera</i> (grapes)	78
<i>Hordeum brevisubulatum</i> (wild barley)	82
<i>Pyrus communis</i> (common pear)	84
<i>Chenopodium rubrum</i> (red goosefoot)	83
<i>Hevea brasiliensis</i> (rubber tree)	84
<i>Vigna radiata</i> (mung bean)	82
<i>Thellungiella salsuginea</i> (Salt-lick mustard)	90
<i>Chara corallina</i> (green algae)	67
<i>Chlamydomonas</i> <i>reinhardtii</i> (algae)	61
Parasites	
<i>Trypanosoma brucei</i> (parasite)	51
<i>Leptospira interrogans</i> (spirochete)	54
<i>Toxoplasma gondii</i> (parasite)	48
<i>Plasmodium falciparum</i> (parasite)	49

[illegible]